

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 126.025 Seconds
(without alignments)
6151.841 Million cell updates/sec

Title: US-10-088-117A-18

Perfect score: 16

Sequence: 1 cbgayatcstrctgcc 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

GenBank:
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 14 | 87.5 | 236 | 11 DM22G6T | Z50523 D. melanoga |
| 3 | 14 | 87.5 | 594 | 6 BD163513 | BD163513 Novel pol |
| 4 | 14 | 87.5 | 594 | 6 AX121396 | AX121396 Sequence |
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| 8 | 14 | 87.5 | 643 | 1 AX209024 | AX209024 Unculture |
| 9 | 14 | 87.5 | 643 | 1 AX209035 | AX209035 Unculture |
| 10 | 14 | 87.5 | 644 | 1 AX325542 | AX325542 Unculture |
| 11 | 14 | 87.5 | 645 | 1 AX552337 | AX552337 Unidentif |
| 12 | 14 | 87.5 | 647 | 1 AX209048 | AX209048 Unculture |
| 13 | 14 | 87.5 | 647 | 1 AX209118 | AX209118 Unculture |
| 14 | 14 | 87.5 | 649 | 1 AX552386 | AX552386 Unidentif |
| 15 | 14 | 87.5 | 650 | 1 AX209084 | AX209084 Unculture |
| 16 | 14 | 87.5 | 650 | 1 AX325520 | AX325520 Unculture |
| 17 | 14 | 87.5 | 650 | 1 AX325522 | AX325522 Unculture |
| 18 | 14 | 87.5 | 650 | 1 AX325562 | AX325562 Unculture |
| 19 | 14 | 87.5 | 650 | 1 AX325585 | AX325585 Unculture |

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|----|----|------|-----|---|----------|--------------------|
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| 22 | 14 | 87.5 | 650 | 1 | AY453365 | AY453365 Unculture |
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| 24 | 14 | 87.5 | 651 | 1 | AY552359 | AY552359 Unidentif |
| 25 | 14 | 87.5 | 651 | 1 | AY552382 | AY552382 Unidentif |
| 26 | 14 | 87.5 | 652 | 1 | AY113805 | AY113805 Unculture |
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| 28 | 14 | 87.5 | 652 | 1 | AY209034 | AY209034 Unculture |
| 29 | 14 | 87.5 | 652 | 1 | AY209133 | AY209133 Unculture |
| 30 | 14 | 87.5 | 652 | 1 | AY453378 | AY453378 Unculture |
| 31 | 14 | 87.5 | 652 | 1 | AY552373 | AY552373 Unidentif |
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| 34 | 14 | 87.5 | 653 | 1 | AY113782 | AY113782 Unculture |
| 35 | 14 | 87.5 | 653 | 1 | AY209027 | AY209027 Unculture |
| 36 | 14 | 87.5 | 653 | 1 | AY209049 | AY209049 Unculture |
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| 38 | 14 | 87.5 | 653 | 1 | AY209055 | AY209055 Unculture |
| 39 | 14 | 87.5 | 653 | 1 | AY209058 | AY209058 Unculture |
| 40 | 14 | 87.5 | 653 | 1 | AY209060 | AY209060 Unculture |
| 41 | 14 | 87.5 | 653 | 1 | AY209073 | AY209073 Unculture |
| 42 | 14 | 87.5 | 653 | 1 | AY209083 | AY209083 Unculture |
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| 44 | 14 | 87.5 | 653 | 1 | AY209103 | AY209103 Unculture |
| 45 | 14 | 87.5 | 653 | 1 | AY209108 | AY209108 Unculture |
| 46 | 14 | 87.5 | 653 | 1 | AY209117 | AY209117 Unculture |
| 47 | 14 | 87.5 | 653 | 1 | AY209120 | AY209120 Unculture |
| 48 | 14 | 87.5 | 653 | 1 | AY209123 | AY209123 Unculture |
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| 50 | 14 | 87.5 | 653 | 1 | AY325537 | AY325537 Unculture |

ALIGNMENTS

RESULT 1
AX098621
LOCUS AX098621 16 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 18 from Patent WO0120030.
ACCESSION AX098621
VERSION AX098621.1 GI:13537882
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Giordano,G., dos Santos,J.P. and Mejean,V.
TITLE Nucleotide sequences derived from genes coding for trimethylamine n-oxide reductase, uses thereof in particular for detecting bacteria
JOURNAL Patent: WO 0120030-A 18 22-MAR-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
Location/Qualifiers
source 1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="amorce PCR"
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Best Local Similarity 100.0%; Pred. No. 3.3e+03; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;
Oy 1 CBGAYATCSTRCTGCC 16
| | | | | | | | | | | | | | | |
Db 1 CBGAYATCSTRCTGCC 16
RESULT 2
DM22G6T/c
LOCUS DM22G6T 236 bp DNA linear STS 17-APR-1996

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 22:48:55 ; Search time 15.9815 Seconds
(without alignments)
5926.580 Million cell updates/sec

Title: US-10-088-117a-18

Perfect score: 16

Sequence: 1 cbgayatcstrtgcc 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : N_Geneseq_16Dec04:*

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2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
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| 2 | 14 | 87.5 | 263 | 7 | AdS65451 Corn seed |
| 3 | 14 | 87.5 | 594 | 5 | Aah66277 C glutami |
| 4 | 14 | 87.5 | 741 | 12 | Adi45730 Corn isop |
| 5 | 14 | 87.5 | 741 | 12 | ADJ44921 Plant cDN |
| 6 | 14 | 87.5 | 883 | 13 | AdS56043 Bacterial |
| 7 | 14 | 87.5 | 1244 | 13 | AdT05004 Haemophil |
| 8 | 14 | 87.5 | 1470 | 11 | AbD03667 Pseudomon |
| 9 | 14 | 87.5 | 1563 | 11 | AbD04037 Pseudomon |
| 10 | 14 | 87.5 | 1896 | 12 | AdM47884 Polynucle |
| 11 | 14 | 87.5 | 1887 | 4 | Aah19221 Human sec |
| 12 | 14 | 87.5 | 1905 | 5 | Aa879304 DNA encod |
| 13 | 14 | 87.5 | 1956 | 13 | AdS56469 Bacterial |
| 14 | 14 | 87.5 | 2130 | 8 | ACA31652 Prokaryot |
| 15 | 14 | 87.5 | 2268 | 8 | ACA31543 Prokaryot |
| 16 | 14 | 87.5 | 2280 | 8 | ACA50924 Prokaryot |
| 17 | 14 | 87.5 | 2328 | 13 | AdT45718 Bacterial |
| 18 | 14 | 87.5 | 2358 | 8 | ACA19185 Prokaryot |
| 19 | 14 | 87.5 | 2358 | 13 | AdS46037 Bacterial |
| 20 | 14 | 87.5 | 2454 | 11 | ACH97441 Klebsiell |

| | | | | | |
|----|------|------|--------|----|--------------------|
| 21 | 14 | 87.5 | 2475 | 4 | AAF79948 |
| 22 | 14 | 87.5 | 2487 | 4 | AAF79943 |
| 23 | 14 | 87.5 | 2503 | 4 | AAF71276 |
| 24 | 14 | 87.5 | 2544 | 4 | AAF79949 |
| 25 | 14 | 87.5 | 2547 | 13 | AdS46046 Bacterial |
| 26 | 14 | 87.5 | 2853 | 5 | AAS72308 |
| 27 | 14 | 87.5 | 2853 | 5 | AAS93061 DNA encod |
| 28 | 14 | 87.5 | 2853 | 5 | AAS92727 DNA encod |
| 29 | 14 | 87.5 | 2853 | 5 | AAS86655 DNA encod |
| 30 | 14 | 87.5 | 3687 | 6 | AdD28410 Bacillus |
| 31 | 14 | 87.5 | 3687 | 13 | AdT48591 Bacterial |
| 32 | 14 | 87.5 | 3712 | 4 | AaH19184 Human sec |
| 33 | 14 | 87.5 | 3741 | 8 | ACA35058 Prokaryot |
| 34 | 14 | 87.5 | 3744 | 4 | AAS56106 Salmoneil |
| 35 | 14 | 87.5 | 3744 | 5 | AaH66279 C glutami |
| 36 | 14 | 87.5 | 3744 | 8 | ACA51923 Prokaryot |
| 37 | 14 | 87.5 | 3846 | 11 | ACH97430 Klebsiell |
| 38 | 14 | 87.5 | 3874 | 10 | ADH13658 C. glutam |
| 39 | 14 | 87.5 | 11275 | 6 | AaH43717 E. coli g |
| 40 | 14 | 87.5 | 98300 | 12 | ADO79403 KIAA0783 |
| 41 | 14 | 87.5 | 110000 | 2 | Continuation (15 o |
| 42 | 14 | 87.5 | 110000 | 6 | ABA90521_14 |
| 43 | 14 | 87.5 | 22587 | 12 | ADO97397 Human can |
| 44 | 14 | 87.5 | 34980 | 5 | AaH68528 C glutami |
| 45 | 14 | 87.5 | 34980 | 13 | ADT05648 Haemophil |
| 46 | 13.2 | 82.5 | 277 | 3 | AAC10817 Human sec |
| 47 | 13.2 | 82.5 | 653 | 10 | ACC79070 Human pan |
| 48 | 13.2 | 82.5 | 763 | 2 | AAS8279 DNA encod |
| 49 | 13.2 | 82.5 | 972 | 5 | AAS82875 DNA encod |
| 50 | 13.2 | 82.5 | 998 | 5 | AAS96227 Human bon |

ALIGNMENTS

RESULT 1

AAF79957
ID AAF79957 standard; DNA; 16 BP.

XX AC AAF79957;

XX DT 11-JUN-2001 (first entry)

XX DE PCR primer used to amplify trimethylamine N-oxide reductase genes.

XX KW torA gene; trimethylamine N-oxide reductase; flesh degradation;

XX KW spoilage bacteria; fish; crustacean; PCR primer; ss.

XX OS Synthetic.

XX PN WO200120030-A2.

XX XX 22-MAR-2001.

XX PD 15-SEP-2000; 2000WO-FR002578.

XX XX 15-SEP-1999; 99FR-00011543.

XX XX (CNRS) CENT NAT RECH SCI.

XX PI Giordano G, Dos Santos J, Mejean V;

XX WPI; 2001-244822/25.

DR Detecting bacteria that cause flesh degradation in fish, for testing
XX freshness, comprises using probes or primers based on the trimethylamine
PT N-oxide reductase system.

XX PS Claim 7; Page 42; 91pp; French.

XX CC PCR primers AAF79951-66 represent PCR primers used to amplify torA and
XX torC genes. TorA and torC are bacterial proteins of the trimethylamine N-
XX oxide reductase system. TorA nucleic acids are used for detecting, in a

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 08:20:11 ; Search time 4.94154 Seconds
(without alignments)
5298.032 Million cell updates

Title: US-10-088-117A-18

Perfect score: 16

Sequence: 1 cbgayatcstrctgcc 16

Scoring table: IDENTITY NUC

Gapop 10.0 : Gapext 1.0

Searched: 1202784 BEGS. 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|---------|-------|----------------------|
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| C 2 | 14 | 87.5 | 601 | 4 | US-09-949-016-159206 |
| C 3 | 14 | 87.5 | 1470 | 4 | US-09-252-991A-2271 |
| C 4 | 14 | 87.5 | 1563 | 4 | US-09-259-931A-2641 |
| C 5 | 14 | 87.5 | 2454 | 4 | US-09-489-039A-3236 |
| C 6 | 14 | 87.5 | 2503 | 4 | US-09-602-777A-277 |
| C 7 | 14 | 87.5 | 3687 | 4 | US-09-891-641-1 |
| C 8 | 14 | 87.5 | 3846 | 4 | US-09-489-039A-3225 |
| C 9 | 14 | 87.5 | 18157 | 4 | US-09-949-016-16193 |
| C 10 | 14 | 87.5 | 1830121 | 4 | US-09-557-884-1 |
| C 11 | 14 | 87.5 | 1830121 | 4 | US-09-643-990A-1 |
| C 12 | 13.2 | 82.5 | 277 | 4 | US-09-513-999C-14892 |
| C 13 | 13.2 | 82.5 | 368 | 4 | US-09-621-976-30 |
| C 14 | 13.2 | 82.5 | 762 | 2 | US-08-822-261-2 |
| C 15 | 13.2 | 82.5 | 762 | 2 | US-09-226-853-2 |
| C 16 | 13.2 | 82.5 | 15853 | 4 | US-09-949-016-12121 |
| C 17 | 13.2 | 82.5 | 15853 | 4 | US-09-949-016-16051 |
| C 18 | 13 | 81.2 | 263 | 4 | US-09-016-434-178 |
| C 19 | 13 | 81.2 | 351 | 4 | US-09-270-767-4863 |
| C 20 | 13 | 81.2 | 351 | 4 | US-09-270-767-20145 |
| C 21 | 13 | 81.2 | 416 | 4 | US-09-544-398B-45 |
| C 22 | 13 | 81.2 | 416 | 4 | US-09-543-771B-45 |
| C 23 | 13 | 81.2 | 440 | 2 | US-08-318-837-2 |
| C 24 | 13 | 81.2 | 601 | 4 | US-09-949-016-42148 |
| C 25 | 13 | 81.2 | 699 | 4 | US-09-902-540-5326 |
| C 26 | 13 | 81.2 | 700 | 4 | US-09-902-540-185 |
| C 27 | 13 | 81.2 | 780 | 3 | US-08-990-823-70 |

ALIGNMENTS

RESULT 1

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US-09-949-016-22155/c
; Sequence 22155, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN
; TITLE OF INVENTION: WITH HUMAN DISEASE,
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22155
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-22155

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Query Match 87.5%; Score 14; DB 4; Length 601;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 12; Conservative 4; Mismatches 0; Indels

Qy 1 CBGAYATCSTRCTGCC 16
 | : | : | : | : | :
Db 63 CGGACATCCTGTCTGCC 48

RESULT 2

US-09-949-016-159206/c
; Sequence 159206, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:25:53 ; Search time 17.0277 Seconds
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5776.400 Million cell updates/sec

Title: US-10-088-117A-18

Perfect score: 16

Sequence: 1 cbgayatcstrtgcc 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications NA:*

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|-------|-------|--------|----|----------------------|
| 1 | 14 | 87.5 | 263 | 9 | US-09-923-876-467 |
| 2 | 14 | 87.5 | 263 | 10 | US-09-923-876-467 |
| 3 | 14 | 87.5 | 594 | 9 | US-09-923-876-467 |
| 4 | 14 | 87.5 | 741 | 17 | US-10-259-194A-661 |
| 5 | 14 | 87.5 | 741 | 17 | US-10-260-238-5921 |
| 6 | 14 | 87.5 | 811 | 18 | US-10-425-115-42253 |
| 7 | 14 | 87.5 | 883 | 17 | US-10-369-493-31717 |
| 8 | 14 | 87.5 | 1696 | 17 | US-10-310-154-302 |
| 9 | 14 | 87.5 | 1696 | 19 | US-10-732-923-246 |
| 10 | 14 | 87.5 | 1956 | 17 | US-10-369-493-32143 |
| 11 | 14 | 87.5 | 2130 | 17 | US-10-282-122A-19522 |

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|----|------|------|---------|----|----------------------|--------------------|
| 12 | 14 | 87.5 | 2268 | 17 | US-10-282-122A-19413 | Sequence 19413, A |
| 13 | 14 | 87.5 | 2280 | 17 | US-10-282-122A-38794 | Sequence 38794, A |
| 14 | 14 | 87.5 | 2328 | 17 | US-10-369-493-44156 | Sequence 44156, A |
| 15 | 14 | 87.5 | 2358 | 17 | US-10-369-493-24467 | Sequence 24467, A |
| 16 | 14 | 87.5 | 2358 | 17 | US-10-282-122A-7055 | Sequence 7055, Ap |
| 17 | 14 | 87.5 | 2547 | 17 | US-10-369-493-24476 | Sequence 24476, A |
| 18 | 14 | 87.5 | 3687 | 9 | US-09-891-641-1 | Sequence 1, Appli |
| 19 | 14 | 87.5 | 3687 | 17 | US-10-369-493-47029 | Sequence 47029, A |
| 20 | 14 | 87.5 | 3687 | 17 | US-10-602-747A-1 | Sequence 1, Appli |
| 21 | 14 | 87.5 | 3687 | 17 | US-10-375-191-1 | Sequence 1, Appli |
| 22 | 14 | 87.5 | 3741 | 17 | US-10-282-122A-22928 | Sequence 22928, A |
| 23 | 14 | 87.5 | 3744 | 9 | US-09-815-242-9743 | Sequence 9743, Ap |
| 24 | 14 | 87.5 | 3744 | 9 | US-09-738-626-1314 | Sequence 1314, Ap |
| 25 | 14 | 87.5 | 3744 | 17 | US-10-282-122A-38793 | Sequence 38793, A |
| 26 | 14 | 87.5 | 11275 | 16 | US-10-240-689-39 | Sequence 39, Appl |
| 27 | 14 | 87.5 | 36401 | 19 | US-10-925-357-1 | Sequence 1, Appli |
| 28 | 14 | 87.5 | 1830121 | 17 | US-10-329-670-1 | Sequence 1, Appli |
| 29 | 14 | 87.5 | 1830121 | 18 | US-10-158-865-1 | Sequence 1, Appli |
| 30 | 14 | 87.5 | 3309400 | 9 | US-09-738-626-1 | Sequence 1, Appli |
| 31 | 13.2 | 82.5 | 653 | 19 | US-10-487-078-125 | Sequence 125, App |
| 32 | 13.2 | 82.5 | 712 | 13 | US-10-027-632-16473 | Sequence 16473, A |
| 33 | 13.2 | 82.5 | 712 | 17 | US-10-027-632-16473 | Sequence 16473, A |
| 34 | 13.2 | 82.5 | 762 | 15 | US-10-316-761-2 | Sequence 2, Appli |
| 35 | 13.2 | 82.5 | 3137 | 13 | US-10-027-632-264695 | Sequence 264695, A |
| 36 | 13.2 | 82.5 | 3137 | 17 | US-10-027-632-264695 | Sequence 264695, A |
| 37 | 13 | 81.2 | 25 | 19 | US-10-719-900-37229 | Sequence 37229, A |
| 38 | 13 | 81.2 | 25 | 19 | US-10-719-900-185408 | Sequence 185408, A |
| 39 | 13 | 81.2 | 47 | 14 | US-10-013-173-16 | Sequence 16, Appl |
| 40 | 13 | 81.2 | 47 | 15 | US-10-150-762-16 | Sequence 16, Appl |
| 41 | 13 | 81.2 | 47 | 15 | US-10-244-821-16 | Sequence 16, Appl |
| 42 | 13 | 81.2 | 141 | 18 | US-10-425-115-95266 | Sequence 95266, A |
| 43 | 13 | 81.2 | 181 | 9 | US-09-867-701-7089 | Sequence 7089, Ap |
| 44 | 13 | 81.2 | 192 | 15 | US-10-156-761-5179 | Sequence 5179, Ap |
| 45 | 13 | 81.2 | 263 | 17 | US-10-305-720-178 | Sequence 178, App |
| 46 | 13 | 81.2 | 302 | 18 | US-10-425-115-12070 | Sequence 12070, A |
| 47 | 13 | 81.2 | 359 | 9 | US-09-917-800A-691 | Sequence 691, App |
| 48 | 13 | 81.2 | 398 | 16 | US-10-029-386-14441 | Sequence 14441, A |
| 49 | 13 | 81.2 | 401 | 9 | US-09-864-761-32357 | Sequence 32357, A |
| 50 | 13 | 81.2 | 414 | 18 | US-10-425-115-87116 | Sequence 87116, A |

ALIGNMENTS

RESULT 1

US-09-923-876-467 ; Sequence 467, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Lalqudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 467
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700156983H1
; US-09-923-876-467

Query Match 87.5%; Score 14; DB 9; Length 263;
Best Local Similarity 75.0%; Pred. No. 6.5e+02;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 07:12:26 ; Search time 107.594 Seconds
(without alignments)
5660.438 Million cell updates/sec

Title: US-10-088-117A-18

Perfect score: 16

Sequence: 1 cbgayatcstrgtgc 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 14 | 87.5 | 188 | 9 | CG733285 |
| 2 | 14 | 87.5 | 219 | 8 | AZ868010 |
| 3 | 14 | 87.5 | 237 | 8 | AZ857279 |
| 4 | 14 | 87.5 | 259 | 1 | A1881564 |
| 5 | 14 | 87.5 | 328 | 8 | AZ755055 |
| 6 | 14 | 87.5 | 363 | 7 | W87131 |
| 7 | 14 | 87.5 | 365 | 4 | BG837422 |
| 8 | 14 | 87.5 | 391 | 7 | W11810 |
| 9 | 14 | 87.5 | 391 | 6 | CD783767 |
| 10 | 14 | 87.5 | 408 | 5 | BY298653 |
| 11 | 14 | 87.5 | 423 | 6 | CD091125 |
| 12 | 14 | 87.5 | 459 | 8 | BH240839 |
| 13 | 14 | 87.5 | 484 | 5 | BZ266837 |
| 14 | 14 | 87.5 | 492 | 1 | A4914387 |
| 15 | 14 | 87.5 | 513 | 8 | B47814 |
| 16 | 14 | 87.5 | 529 | 8 | AQ434937 |
| 17 | 14 | 87.5 | 537 | 6 | CD793456 |
| 18 | 14 | 87.5 | 550 | 5 | BP339064 |
| 19 | 14 | 87.5 | 570 | 9 | CR205324 |
| 20 | 14 | 87.5 | 578 | 6 | CB536706 |
| 21 | 14 | 87.5 | 586 | 6 | CD780356 |
| 22 | 14 | 87.5 | 589 | 6 | CD785404 |
| 23 | 14 | 87.5 | 594 | 7 | C0531075 |
| 24 | 14 | 87.5 | 603 | 7 | C0530140 |

| | | | | | |
|----|----|------|-----|---|----------|
| 25 | 14 | 87.5 | 611 | 6 | CD793634 |
| 26 | 14 | 87.5 | 614 | 8 | AQ418346 |
| 27 | 14 | 87.5 | 629 | 9 | CNS03K21 |
| 28 | 14 | 87.5 | 636 | 4 | BG859034 |
| 29 | 14 | 87.5 | 641 | 8 | BH240856 |
| 30 | 14 | 87.5 | 643 | 9 | CR836654 |
| 31 | 14 | 87.5 | 659 | 6 | CD727887 |
| 32 | 14 | 87.5 | 663 | 1 | AU171960 |
| 33 | 14 | 87.5 | 669 | 1 | AU168386 |
| 34 | 14 | 87.5 | 676 | 8 | BH240857 |
| 35 | 14 | 87.5 | 683 | 7 | CV031060 |
| 36 | 14 | 87.5 | 687 | 5 | BQ157381 |
| 37 | 14 | 87.5 | 694 | 8 | BH240937 |
| 38 | 14 | 87.5 | 697 | 7 | C0525966 |
| 39 | 14 | 87.5 | 698 | 9 | CG108657 |
| 40 | 14 | 87.5 | 715 | 6 | CD787450 |
| 41 | 14 | 87.5 | 729 | 6 | CD787993 |
| 42 | 14 | 87.5 | 734 | 4 | B0709624 |
| 43 | 14 | 87.5 | 735 | 8 | BH240782 |
| 44 | 14 | 87.5 | 738 | 7 | CF698998 |
| 45 | 14 | 87.5 | 740 | 1 | AJ801168 |
| 46 | 14 | 87.5 | 746 | 6 | CD796273 |
| 47 | 14 | 87.5 | 756 | 6 | CD780487 |
| 48 | 14 | 87.5 | 757 | 9 | CG134378 |
| 49 | 14 | 87.5 | 764 | 5 | BX926800 |
| 50 | 14 | 87.5 | 770 | 7 | C0060110 |

ALIGNMENTS

CG733285 188 bp DNA linear GSS 20-OCT-2003
1119155C11.y1.1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.
CG733285
CG733285.1 GI:37775777
GSS:
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 188)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1119155 row: 6
Class: transposon-tagged.
Location/Qualifiers
1. 188
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/lab_host="DH10B"
/dev_stage="adult"
/tissue_type="leaf"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site: 1: BamHI, Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web

GenCore version 5.1.6

Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 157.531 Seconds

(without alignments)
6151.841 Million cell updates/sec

Title: US-10-088-117A-19

Perfect score: 20

Sequence: 1 ggmgaytaytcacmggygc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pi.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 17.2 | 86.0 | 20 | 6 | AX098622 Sequence |
| 2 | 17.2 | 86.0 | 1998 | 6 | AR387097 Sequence |
| 3 | 17.2 | 86.0 | 2385 | 6 | AR387009 Sequence |
| 4 | 17.2 | 86.0 | 2475 | 6 | AX098610 Sequence |
| 5 | 17.2 | 86.0 | 2486 | 6 | AX098605 Sequence |
| 6 | 17.2 | 86.0 | 2487 | 6 | AX098604 Sequence |
| 7 | 17.2 | 86.0 | 2487 | 6 | AX098606 Sequence |
| 8 | 17.2 | 86.0 | 2490 | 1 | SPU5974 |
| 9 | 17.2 | 86.0 | 2523 | 6 | AX098609 Sequence |
| 10 | 17.2 | 86.0 | 2540 | 1 | PCDSTNORG |
| 11 | 17.2 | 86.0 | 2544 | 6 | AX098612 Sequence |
| 12 | 17.2 | 86.0 | 3235 | 1 | AF134212 |
| 13 | 17.2 | 86.0 | 4680 | 1 | AF134212 Helicobac |
| 14 | 17.2 | 86.0 | 5637 | 1 | U49506 Rhodobacter |
| 15 | 17.2 | 86.0 | 5637 | 1 | U49506 Rhodobacter |
| 16 | 17.2 | 86.0 | 6915 | 1 | AX006085 Shewanell |
| 17 | 17.2 | 86.0 | 7990 | 1 | AF018236 |
| 18 | 17.2 | 86.0 | 10726 | 1 | AE015567 Shewanell |
| 19 | 17.2 | 86.0 | 13067 | 1 | AE015128 Shigella |
| 19 | 17.2 | 86.0 | 18252 | 1 | D90737 Escherichia |

| | | | | | |
|----|------|-------|--------|---|------------|
| 20 | 17.2 | 86.0 | 19650 | 1 | D90736 |
| 21 | 17.2 | 86.0 | 22072 | 1 | AE008869 |
| 22 | 17.2 | 86.0 | 110000 | 1 | U00096.10 |
| 23 | 17.2 | 86.0 | 190822 | 2 | AC051613 |
| 24 | 17.2 | 86.0 | 265050 | 1 | AL627281 |
| 25 | 17.2 | 86.0 | 272545 | 2 | AC090533 |
| 26 | 17.2 | 86.0 | 292504 | 1 | AE016981 |
| 27 | 17.2 | 86.0 | 300102 | 1 | AE016847 |
| 28 | 17.2 | 86.0 | 301276 | 1 | AE016758 |
| 29 | 17.2 | 86.0 | 302212 | 1 | AE017147 |
| 30 | 16.4 | 82.0 | 21 | 6 | AX098615 |
| 31 | 16.4 | 82.0 | 10968 | 1 | AE004270 |
| 32 | 16.2 | 81.0 | 408 | 6 | CQ442063 |
| 33 | 16 | 80.0 | 3337 | 1 | ECOBISCASD |
| 34 | 16 | 80.0 | 10593 | 1 | AE015366 |
| 35 | 16 | 80.0 | 10715 | 1 | AE006216 |
| 36 | 16 | 80.0 | 11006 | 1 | AE005582 |
| 37 | 16 | 80.0 | 11289 | 1 | AE005293 |
| 38 | 16 | 80.0 | 22418 | 1 | AE008878 |
| 39 | 16 | 80.0 | 110000 | 1 | U00096.37 |
| 40 | 16 | 80.0 | 154978 | 2 | AC073952 |
| 41 | 16 | 80.0 | 173938 | 2 | AC148536 |
| 42 | 16 | 80.0 | 200491 | 9 | AC007249 |
| 43 | 16 | -80.0 | 225419 | 1 | ECUW76 |
| 44 | 16 | 80.0 | 245050 | 1 | AL627280 |
| 45 | 16 | 80.0 | 267888 | 1 | AP002565 |
| 46 | 16 | 80.0 | 289816 | 1 | AP016992 |
| 47 | 16 | 80.0 | 299130 | 1 | AP005077 |
| 48 | 16 | 80.0 | 300592 | 1 | AE016846 |
| 49 | 16 | 80.0 | 301660 | 1 | AE016768 |
| 50 | 16 | 80.0 | 327773 | 1 | AP002554 |

ALIGNMENTS

RESULT 1

AX098622

LOCUS

DEFINITION

AX098622

ACCESSION

AX098622.1

VERSION

AX098622.1

KEYWORDS

SYNTHETIC CONSTRUCT

ORGANISM

SYNTHETIC CONSTRUCT

REFERENCE

1

Giordano, G., dos Santos, J. P. and Mejean, V.

Nucleotide sequences derived from genes coding for trimethylamine

n-oxide reductase, uses thereof in particular for detecting

bacteria

Patent: WO 0120030-A 19 22-MAR-2001.

CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

JOURNAL

LOCATION/QUALIFIERS

1. 20

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="amorce PCR"

FEATURES

source

1. 20

ORIGIN

Query Match

Best Local Similarity

Matches

20; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Length 20;

Pred. No. 1e+03;

Score 86.0%;

1 GGMGAYTAYTCBACMGGYGC 20

|||||

1 GGMGAYTAYTCBACMGGYGC 20

|||||

RESULT 2

AR387097/c

LOCUS

1998 bp

DNA

linear

PAT 18-DEC-2003

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 1, 2005, 22:48:55 ; Search time 19.9769 Seconds
(without alignments)
5926.580 Million cell updates/sec

Title: US-10-088-117a-19
Perfect score: 20
Sequence: 1 gmgaytactcagcmgygc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

- Database : N_Geneseq_16Dec04.*
- 1: Geneseq1980s.*
 - 2: Geneseq1990s.*
 - 3: Geneseq2000s.*
 - 4: Geneseq2001as.*
 - 5: Geneseq2001bs.*
 - 6: Geneseq2002as.*
 - 7: Geneseq2002bs.*
 - 8: Geneseq2003as.*
 - 9: Geneseq2003bs.*
 - 10: Geneseq2003cs.*
 - 11: Geneseq2003ds.*
 - 12: Geneseq2004as.*
 - 13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 17.2 | 86.0 | 20 | 4 | Aaf79958 PCR prime |
| 2 | 17.2 | 86.0 | 1998 | 11 | Ach98031 Klebsiell |
| 3 | 17.2 | 86.0 | 2385 | 11 | Ach97943 Klebsiell |
| 4 | 17.2 | 86.0 | 2475 | 4 | Aaf79948 Nucleotid |
| 5 | 17.2 | 86.0 | 2486 | 4 | Aaf79944 Nucleotid |
| 6 | 17.2 | 86.0 | 2487 | 4 | Aaf79945 Nucleotid |
| 7 | 17.2 | 86.0 | 2487 | 4 | Aaf79943 Nucleotid |
| 8 | 17.2 | 86.0 | 2523 | 4 | Aaf79947 Nucleotid |
| 9 | 17.2 | 86.0 | 2544 | 4 | Aaf79949 Nucleotid |
| 10 | 17.2 | 86.0 | 2547 | 13 | AdS46046 Bacterial |
| 11 | 17.2 | 86.0 | 11275 | 6 | Aah43717 E. coli 9 |
| 12 | 16.4 | 82.0 | 21 | 4 | Aaf79951 PCR prime |
| 13 | 16.2 | 81.0 | 408 | 6 | Abn19673 Human ORF |
| 14 | 16 | 80.0 | 1455 | 5 | Aas86797 DNA encod |
| 15 | 16 | 80.0 | 2220 | 13 | AdT48846 Bacterial |
| 16 | 15.6 | 78.0 | 780 | 11 | Abd01207 Klebsiell |
| 17 | 15.6 | 78.0 | 2120 | 13 | AdS58851 Bacterial |
| 18 | 15.6 | 78.0 | 2556 | 8 | ACA38838 |
| 19 | 15.6 | 78.0 | 2637 | 12 | AdL03795 DNA encod |
| 20 | 15.6 | 78.0 | 2742 | 13 | AdR85388 Aspergill |

| | | | | | |
|----|------|------|--------|----|----------|
| 21 | 15.6 | 78.0 | 2809 | 13 | ADR84801 |
| 22 | 15.6 | 78.0 | 8809 | 13 | ADR84214 |
| 23 | 15.6 | 78.0 | 23210 | 4 | AAF28530 |
| 24 | 15.2 | 76.0 | 1883 | 5 | ABV23467 |
| 25 | 15.2 | 76.0 | 1883 | 5 | ABV23113 |
| 26 | 15.2 | 76.0 | 1883 | 5 | ABV29325 |
| 27 | 15.2 | 76.0 | 2448 | 13 | ADS46130 |
| 28 | 15.2 | 76.0 | 7410 | 5 | AAS74643 |
| 29 | 15.2 | 76.0 | 7410 | 5 | AAS93051 |
| 30 | 15.2 | 76.0 | 10161 | 5 | AAS93288 |
| 31 | 15 | 75.0 | 655 | 3 | AAF07946 |
| 32 | 15 | 75.0 | 980 | 13 | ADR62409 |
| 33 | 15 | 75.0 | 1435 | 13 | ADR64626 |
| 34 | 15 | 75.0 | 3291 | 12 | ADO00942 |
| 35 | 15 | 75.0 | 5404 | 4 | ABL14953 |
| 36 | 15 | 75.0 | 12870 | 4 | ABL14952 |
| 37 | 14.8 | 74.0 | 1242 | 5 | AAH67611 |
| 38 | 14.8 | 74.0 | 349980 | 5 | AAH68532 |
| 39 | 14.6 | 73.0 | 486 | 8 | ABZ54835 |
| 40 | 14.6 | 73.0 | 523 | 5 | ABV35656 |
| 41 | 14.6 | 73.0 | 523 | 5 | ABV44461 |
| 42 | 14.6 | 73.0 | 595 | 13 | ADR13125 |
| 43 | 14.6 | 73.0 | 617 | 13 | ADR13124 |
| 44 | 14.6 | 73.0 | 782 | 5 | ABV14577 |
| 45 | 14.6 | 73.0 | 988 | 6 | ABL89972 |
| 46 | 14.6 | 73.0 | 1248 | 13 | ADR13562 |
| 47 | 14.6 | 73.0 | 1542 | 10 | ADB78939 |
| 48 | 14.6 | 73.0 | 2642 | 4 | AAK94318 |
| 49 | 14.6 | 73.0 | 2642 | 12 | ADL30960 |
| 50 | 14.6 | 73.0 | 2732 | 13 | ADR08163 |

ALIGNMENTS

RESULT 1

AAF79958
ID AAF79958 standard; DNA; 20 BP.

XX AAF79958;

XX 11-JUN-2001 (first entry)

DE PCR primer used to amplify trimethylamine N-oxide reductase genes.

XX torA gene; trimethylamine N-oxide reductase; flesh degradation;

KW spoilage bacteria; fish; crustacean; PCR primer; ss.

XX Synthetic.

XX WO200120030-A2.

XX 22-MAR-2001.

XX 15-SEP-2000; 2000WO-FR002578.

XX 15-SEP-1999; 99FR-00011543.

XX (CNRS) CENT NAT RECH SCI.

XX Giordano G, Dos Santos J, Mejean V;

XX WPI; 2001-244822/25.

XX Detecting bacteria that cause flesh degradation in fish, for testing
PT freshness, comprises using probes or primers based on the trimethylamine
PT N-oxide reductase system.
XX Claim 7; Page 42; 91pp; French.
XX PCR primers AAF79951-66 represent PCR primers used to amplify torA and
torC genes. TorA and torC are bacterial proteins of the trimethylamine N-
oxide reductase system. TorA nucleic acids are used for detecting, in a

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 08:20:11 ; Search time 6.17692 Seconds
(without alignments)
5298.032 Million cell updates/sec

Title: US-10-088-117A-19

Perfect score: 20

Sequence: 1 gmgaytaytcacmggyc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Issued Patents NA.*

- 1: /cgm2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgm2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgm2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgm2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgm2_6/ptodata/1/ina/PTUS_COMB.seq.*
- 6: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|---------|-------|----------------------|
| c 1 | 17.2 | 86.0 | 1998 | 4 | US-09-489-039A-3826 |
| c 2 | 17.2 | 86.0 | 2385 | 4 | US-09-489-039A-3738 |
| c 3 | 15.6 | 78.0 | 780 | 4 | US-09-489-039A-6982 |
| c 4 | 15.6 | 78.0 | 2637 | 4 | US-09-540-236-1481 |
| c 5 | 15.6 | 78.0 | 23210 | 4 | US-09-596-002-17 |
| c 6 | 14.4 | 72.0 | 303 | 4 | US-09-513-999C-11097 |
| c 7 | 14.4 | 72.0 | 312 | 3 | US-09-060-756-506 |
| c 8 | 14.4 | 72.0 | 312 | 4 | US-09-670-314-506 |
| c 9 | 14.4 | 72.0 | 459 | 4 | US-09-489-039A-6694 |
| c 10 | 14.4 | 72.0 | 1752 | 4 | US-09-489-039A-6747 |
| c 11 | 14.4 | 72.0 | 82125 | 4 | US-09-949-016-13517 |
| c 12 | 14.4 | 72.0 | 82125 | 4 | US-09-949-016-13518 |
| c 13 | 14.4 | 72.0 | 135030 | 4 | US-09-949-016-14896 |
| c 14 | 14.4 | 72.0 | 251672 | 4 | US-09-949-016-17296 |
| c 15 | 14.4 | 72.0 | 251682 | 4 | US-09-949-016-11973 |
| c 16 | 14.4 | 72.0 | 4403765 | 3 | US-09-103-840A-2 |
| c 17 | 14.4 | 72.0 | 4411529 | 3 | US-09-103-840A-1 |
| c 18 | 14.2 | 71.0 | 2294 | 4 | US-09-270-767-10469 |
| c 19 | 14.2 | 71.0 | 1230025 | 4 | US-09-198-452A-1 |
| c 20 | 14.2 | 71.0 | 1230230 | 4 | US-09-438-185A-1 |
| c 21 | 14.0 | 70.0 | 93 | 3 | US-09-952-793-269 |
| c 22 | 14.0 | 70.0 | 93 | 3 | US-09-849-928-269 |
| c 23 | 14.0 | 70.0 | 93 | 5 | PCT-US96-09455A-269 |
| c 24 | 14.0 | 70.0 | 281 | 4 | US-09-513-999C-12276 |
| c 25 | 14.0 | 70.0 | 458 | 4 | US-09-270-767-12137 |
| c 26 | 14.0 | 70.0 | 597 | 4 | US-09-252-991A-8183 |
| c 27 | 14.0 | 70.0 | 601 | 4 | US-09-949-016-20773 |

| | | | | | | |
|------|----|------|-------|---|---------------------|-------------------|
| c 28 | 14 | 70.0 | 601 | 4 | US-09-949-016-20774 | Sequence 20774, A |
| c 29 | 14 | 70.0 | 601 | 4 | US-09-949-016-96202 | Sequence 96202, A |
| c 30 | 14 | 70.0 | 601 | 4 | US-09-949-016-96203 | Sequence 96203, A |
| c 31 | 14 | 70.0 | 601 | 4 | US-09-949-016-96204 | Sequence 96204, A |
| c 32 | 14 | 70.0 | 954 | 4 | US-10-043-238-2 | Sequence 2, Appli |
| c 33 | 14 | 70.0 | 1101 | 4 | US-09-252-991A-5955 | Sequence 5955, Ap |
| c 34 | 14 | 70.0 | 1287 | 4 | US-09-489-039A-123 | Sequence 123, App |
| c 35 | 14 | 70.0 | 1368 | 4 | US-09-902-540-7420 | Sequence 7420, Ap |
| c 36 | 14 | 70.0 | 1383 | 4 | US-09-252-991A-1213 | Sequence 1213, Ap |
| c 37 | 14 | 70.0 | 1503 | 4 | US-09-252-991A-7970 | Sequence 7970, Ap |
| c 38 | 14 | 70.0 | 1773 | 4 | US-09-489-039A-241 | Sequence 241, App |
| c 39 | 14 | 70.0 | 2262 | 4 | US-09-252-991A-1353 | Sequence 1353, Ap |
| c 40 | 14 | 70.0 | 2418 | 4 | US-09-252-991A-1251 | Sequence 1251, Ap |
| c 41 | 14 | 70.0 | 2552 | 4 | US-09-270-767-15247 | Sequence 15247, A |
| c 42 | 14 | 70.0 | 2659 | 3 | US-09-029-267-19 | Sequence 19, Appl |
| c 43 | 14 | 70.0 | 3840 | 4 | US-09-489-039A-6431 | Sequence 6431, Ap |
| c 44 | 14 | 70.0 | 4171 | 4 | US-09-687-422-3 | Sequence 3, Appli |
| c 45 | 14 | 70.0 | 7317 | 4 | US-09-902-540-715 | Sequence 715, App |
| c 46 | 14 | 70.0 | 8157 | 1 | US-08-358-160-65 | Sequence 65, Appl |
| c 47 | 14 | 70.0 | 8578 | 4 | US-09-902-540-871 | Sequence 871, App |
| c 48 | 14 | 70.0 | 8584 | 1 | US-08-358-160-66 | Sequence 66, Appl |
| c 49 | 14 | 70.0 | 8590 | 1 | US-08-358-160-70 | Sequence 70, Appl |
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ALIGNMENTS

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; Sequence 3826, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3826
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-3826

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Best Local Similarity 70.0%; Pred. No. 9.6;
Matches 14; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-489-039A-3738
; Sequence 3738, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3738
; LENGTH: 2385

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(without alignments)
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Listing first 50 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 7 | 15.6 | 78.0 | 2556 | 17 | US-10-282-122A-26708 Sequence 26708, A |
| 8 | 15.6 | 78.0 | 3201 | 18 | US-10-437-963-54673 Sequence 54673, A |
| 9 | 15.6 | 78.0 | 23210 | 17 | US-10-672-787-17 Sequence 17, Appl |
| 10 | 15.6 | 78.0 | 2731748 | 18 | US-10-297-465A-1 Sequence 1, Appl |
| 11 | 15.2 | 76.0 | 1883 | 18 | US-10-357-930-23456 Sequence 23456, A |

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| 15 | 15 | 75.0 | 255 | 18 | US-10-437-963-75824 | Sequence 75824, A |
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| 17 | 15 | 75.0 | 980 | 18 | US-10-767-795-3190 | Sequence 3190, App |
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| 20 | 14.8 | 74.0 | 1242 | 9 | US-09-738-626-2646 | Sequence 2646, App |
| 21 | 14.8 | 74.0 | 3309400 | 9 | US-09-738-626-1 | Sequence 1, Appl |
| 22 | 14.6 | 73.0 | 314 | 18 | US-10-425-115-3928 | Sequence 3928, A |
| 23 | 14.6 | 73.0 | 347 | 17 | US-10-424-599-98600 | Sequence 98600, A |
| 24 | 14.6 | 73.0 | 359 | 18 | US-10-425-115-184059 | Sequence 184059, A |
| 25 | 14.6 | 73.0 | 523 | 18 | US-10-357-930-35674 | Sequence 35674, A |
| 26 | 14.6 | 73.0 | 523 | 18 | US-10-357-930-44480 | Sequence 44480, A |
| 27 | 14.6 | 73.0 | 657 | 18 | US-10-767-701-4569 | Sequence 4569, App |
| 28 | 14.6 | 73.0 | 668 | 18 | US-10-425-115-178403 | Sequence 178403, A |
| 29 | 14.6 | 73.0 | 767 | 18 | US-10-767-701-5491 | Sequence 5491, App |
| 30 | 14.6 | 73.0 | 776 | 13 | US-10-027-632-32434 | Sequence 32434, A |
| 31 | 14.6 | 73.0 | 776 | 17 | US-10-027-632-32434 | Sequence 32434, A |
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| 39 | 14.6 | 73.0 | 986 | 17 | US-10-264-237-534 | Sequence 534, App |
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| 43 | 14.6 | 73.0 | 3006 | 19 | US-10-509-307-7 | Sequence 7, Appl |
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Sequence 24476, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 24476
LENGTH: 2547
TYPE: DNA
ORGANISM: Escherichia coli
US-10-369-493-24476

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Best Local Similarity 70.0%; Pred. No. 20;
Matches 14; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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8: gb_gse1:*

9: gb_gse2:*

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SUMMARIES

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| C 6 | 17.2 | 86.0 | 794 | 9 | CL669134 |
| C 7 | 17.2 | 86.0 | 799 | 8 | BH388945 |
| C 8 | 17.2 | 86.0 | 812 | 9 | CL671059 |
| C 9 | 16.4 | 82.0 | 385 | 2 | AW226349 |
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| C 11 | 16 | 80.0 | 795 | 9 | CW531185 |
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ALIGNMENTS

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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BG456299 GI:13379624
EST.
Medicago truncatula (barrel medic)

Medicago truncatula
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

1 (bases 1 to 684)
Lin, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)

Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380

Email: mharrison@noble.org
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FEATURES
source

GenCore version 5.1.6
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SUMMARIES

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| 10 | 17.6 | 88.0 | 2544 | 6 | AX098612 Sequence |
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ALIGNMENTS

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| RESULT 1 | AX098623 | Sequence 20 from Patent WO0120030. | 20 bp | DNA | linear | PAT 02-APR-2001 |
| LOCUS | AX098623 | Sequence 20 from Patent WO0120030. | | | | |
| DEFINITION | AX098623 | Sequence 20 from Patent WO0120030. | | | | |
| ACCESSION | AX098623.1 | GI:13537884 | | | | |
| VERSION | AX098623.1 | GI:13537884 | | | | |
| KEYWORDS | | synthetic construct | | | | |
| SOURCE | | other sequences; artificial sequences. | | | | |
| ORGANISM | | Giordano, G., dos Santos, J. P. and Mejean, V. | | | | |
| REFERENCE | | Nucleotide sequences derived from genes coding for trimethylamine | | | | |
| AUTHORS | | n-oxide reductase, uses thereof in particular for detecting | | | | |
| TITLE | | bacteria | | | | |
| JOURNAL | | Patent: WO 0120030-A 20 22-MAR-2001; | | | | |
| FEATURES | | CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR) | | | | |
| source | | Location/Qualifiers | | | | |
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| ORIGIN | | | | | | |
| Query Match | | 88.0%; Score 17.6; DB 6; Length 20; | | | | |
| Best Local Similarity | | 100.0%; Pred. No. 87; | | | | |
| Matches | | 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | |
| QY | | 1 TWYGARCGYAACGAYMTCGA 20 | | | | |
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| Db | | 1 TWYGARCGYAACGAYMTCGA 20 | | | | |
| | | | | | | |
| RESULT 2 | | | | | | |
| RSU25037 | | | | | | |
| LOCUS | | | | | | |

linear BCT 16-APR-1998

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 22:48:55 ; Search time 19.9769 Seconds
(without alignments)
5926.580 Million cell updates/sec

Title: US-10-088-117A-20
Perfect score: 20
Sequence: 1 twygarcyaaacgamtgca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
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- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 17.6 | 88.0 | 20 | AA779959 | Aaf79959 PCR prime |
| 2 | 17.6 | 88.0 | 812 | ABQ39018 | Abq39018 Oligonucleotide |
| 3 | 17.6 | 88.0 | 812 | ABQ39019 | Abq39019 Oligonucleotide |
| 4 | 17.6 | 88.0 | 2475 | AA779948 | Aaf79948 Nucleotide |
| 5 | 17.6 | 88.0 | 2486 | AA779944 | Aaf79944 Nucleotide |
| 6 | 17.6 | 88.0 | 2487 | AA779945 | Aaf79945 Nucleotide |
| 7 | 17.6 | 88.0 | 2487 | AA779943 | Aaf79943 Nucleotide |
| 8 | 17.6 | 88.0 | 2523 | AA779947 | Aaf79947 Nucleotide |
| 9 | 17.6 | 88.0 | 2544 | AA779949 | Aaf79949 Nucleotide |
| 10 | 17.6 | 88.0 | 2547 | ADS46046 | Ads46046 Bacterial |
| 11 | 17.6 | 88.0 | 2853 | AA772908 | Aas72908 DNA encod |
| 12 | 17.6 | 88.0 | 2853 | AA772906 | Aas72906 DNA encod |
| 13 | 17.6 | 88.0 | 2853 | AA772927 | Aas72927 DNA encod |
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| 15 | 17.6 | 88.0 | 11275 | AA772927 | Aas72927 DNA encod |
| 16 | 16.6 | 83.0 | 4689 | AA772927 | Aas72927 DNA encod |
| 17 | 16.6 | 83.0 | 110000 | AA772927 | Aas72927 DNA encod |
| 18 | 16.6 | 83.0 | 110000 | AA772927 | Aas72927 DNA encod |
| 19 | 16.4 | 82.0 | 1520 | ABQ44401 | Abq44401 Oligonucleotide |
| 20 | 16.4 | 82.0 | 1520 | ABQ44400 | Abq44400 Oligonucleotide |

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| C 21 | 16 | 80.0 | 174 | 4 | ABL23039 | AbL23039 Drosophil |
| C 22 | 16 | 80.0 | 547 | 6 | ABQ32142 | Abq32142 Oligonucleotide |
| C 23 | 16 | 80.0 | 547 | 6 | ABQ32143 | Abq32143 Oligonucleotide |
| C 24 | 16 | 80.0 | 825 | 6 | ABQ69937 | Abq69937 Listeria |
| C 25 | 16 | 80.0 | 825 | 6 | ABQ67924 | Abq67924 Listeria |
| C 26 | 16 | 80.0 | 1080 | 4 | AAH52069 | Aah52069 Mycobacte |
| C 27 | 16 | 80.0 | 1989 | 6 | AAH68052 | Aah68052 Streptoco |
| C 28 | 16 | 80.0 | 2099 | 6 | ABQ69134 | Abq69134 Listeria |
| C 29 | 16 | 80.0 | 2544 | 4 | ABL23038 | AbL23038 Drosophil |
| C 30 | 16 | 80.0 | 3558 | 6 | ABQ70946 | Abq70946 Listeria |
| C 31 | 16 | 80.0 | 4122 | 4 | ABL06394 | AbL06394 Drosophil |
| C 32 | 16 | 80.0 | 5397 | 4 | ABL08196 | AbL08196 Drosophil |
| C 33 | 16 | 80.0 | 110000 | 4 | AA199682_36 | Continuation (37 o |
| C 34 | 16 | 80.0 | 110000 | 4 | AA199683_36 | Continuation (37 o |
| C 35 | 16 | 80.0 | 110000 | 6 | ABN71527_14 | Continuation (15 o |
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| C 37 | 15.6 | 78.0 | 471 | 11 | ABD17626 | Abd17626 Pseudomon |
| C 38 | 15.6 | 78.0 | 544 | 6 | ABQ17749 | Abq17749 Oligonucleotide |
| C 39 | 15.6 | 78.0 | 544 | 6 | ABQ17748 | Abq17748 Oligonucleotide |
| C 40 | 15.6 | 78.0 | 963 | 11 | ABD17764 | Abd17764 Pseudomon |
| C 41 | 15.6 | 78.0 | 1557 | 11 | ABD17520 | Abd17520 Pseudomon |
| C 42 | 15.6 | 78.0 | 1563 | 11 | ABD17874 | Abd17874 Pseudomon |
| C 43 | 15.6 | 78.0 | 2328 | 13 | ADT45718 | Adt45718 Bacterial |
| C 44 | 15.4 | 77.0 | 25 | 4 | AA779953 | Aaf79953 PCR prime |
| C 45 | 15.4 | 77.0 | 327 | 6 | ABN18330 | Abn18330 Human ORF |
| C 46 | 15.4 | 77.0 | 1008 | 8 | ACA26292 | ACA26292 Prokaryot |
| C 47 | 15.4 | 77.0 | 1128 | 10 | ADC52112 | Adc52112 DNA encod |
| C 48 | 15.4 | 77.0 | 1202 | 4 | ABL53352 | AbL53352 Mushroo |
| C 49 | 15.4 | 77.0 | 1202 | 5 | ABL53444 | AbL53444 Glycero |
| C 50 | 15.4 | 77.0 | 2084 | 4 | ABL26475 | AbL26475 Drosophil |

ALIGNMENTS

RESULT 1

AA779959
ID AAF79959 standard; DNA; 20 BP.

AC AAF79959;

DT 11-JUN-2001 (first entry)

DE PCR primer used to amplify trimethylamine N-oxide reductase genes.

KW torA gene; trimethylamine N-oxide reductase; flesh degradation;

KW spoilage bacteria; fish; crustacean; PCR primer; ss.

OS Synthetic.

PN WO200120030-A2.

PD 22-MAR-2001.

XX 15-SEP-2000; 2000WO-FR002578.

XX 15-SEP-1999; 99FR-00011543.

PA (CNRS) CENT NAT RECH SCI.

PI Giordano G, Dos Santos J, Mejean V;

DR WPI; 2001-244822/25.

XX Detecting bacteria that cause flesh degradation in fish, for testing
PT freshness, comprises using probes or primers based on the trimethylamine
N-oxide reductase system.

PS Claim 7; Page 42; 91pp; French.

XX PCR primers AAF79951-66 represent PCR primers used to amplify torA and
torC genes. TorA and torC are bacterial proteins of the trimethylamine N-
oxide reductase system. TorA nucleic acids are used for detecting, in a

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------------------|-------------------|
| C 1 | 17.6 | 88.0 | 812 | 18 | US-10-363-345A-25609 | Sequence 25609, A |
| C 2 | 17.6 | 88.0 | 812 | 18 | US-10-363-345A-25610 | Sequence 25610, A |
| C 3 | 17.6 | 88.0 | 812 | 19 | US-10-363-483A-25609 | Sequence 25609, A |
| C 4 | 17.6 | 88.0 | 812 | 19 | US-10-363-483A-25610 | Sequence 25610, A |
| C 5 | 17.6 | 88.0 | 2547 | 17 | US-10-369-493-24476 | Sequence 24476, A |
| C 6 | 17.6 | 88.0 | 12175 | 16 | US-10-240-689-39 | Sequence 39, Appl |
| C 7 | 16.6 | 83.0 | 4689 | 17 | US-10-282-122A-33564 | Sequence 33564, A |
| C 8 | 16.4 | 82.0 | 204 | 18 | US-10-425-115-8983 | Sequence 8983, Ap |
| C 9 | 16.4 | 82.0 | 1520 | 18 | US-10-363-345A-30991 | Sequence 30991, A |
| C 10 | 16.4 | 82.0 | 1520 | 18 | US-10-363-345A-30992 | Sequence 30992, A |
| C 11 | 16.4 | 82.0 | 1520 | 19 | US-10-363-483A-30991 | Sequence 30991, A |

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 07:12:26 ; Search time 134.492 Seconds
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Perfect score: 20
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 190321134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

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- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gss1.*
- 9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 3 | 16.6 | 83.0 | 522 | 7 | CF843239 PSHB024XF |
| 4 | 16.6 | 83.0 | 608 | 7 | CF843217 PSHB024XE |
| 5 | 16.6 | 83.0 | 712 | 7 | CF841741 PSHB015XM |
| 6 | 16.4 | 82.0 | 673 | 7 | CF638575 D04 C04 F |
| 7 | 16.4 | 82.0 | 736 | 7 | CO147437 EST822490 |
| 8 | 16 | 80.0 | 353 | 4 | BG955182 CW4-CT065 |
| 9 | 16 | 80.0 | 382 | 9 | CL879226 abf38b01. |
| 10 | 16 | 80.0 | 430 | 6 | CD061642 |
| 11 | 16 | 80.0 | 431 | 6 | CD061662 |
| 12 | 16 | 80.0 | 443 | 6 | CD061564 |
| 13 | 16 | 80.0 | 443 | 7 | CO320509 EK285913 |
| 14 | 16 | 80.0 | 474 | 6 | CD870126 AZ02.1131 |
| 15 | 16 | 80.0 | 493 | 5 | BP092642 |
| 16 | 16 | 80.0 | 510 | 4 | BG653512 sad58c08. |
| 17 | 16 | 80.0 | 514 | 9 | TA114G02Q |
| 18 | 16 | 80.0 | 534 | 7 | CF760096 DSAF1.55 |
| 19 | 16 | 80.0 | 548 | 4 | BF624576 RHG4158.5 |
| 20 | 16 | 80.0 | 555 | 4 | BI510862 B8160003B |
| 21 | 16 | 80.0 | 594 | 8 | BH766340 BMBAC341A |
| 22 | 16 | 80.0 | 604 | 6 | CA065149 SCACAD103 |
| 23 | 16 | 80.0 | 612 | 8 | BH768548 BMBAC360F |
| 24 | 16 | 80.0 | 646 | 6 | CA083457 SCEPAM201 |

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| 25 | 16 | 80.0 | 684 | 8 | BH002877 |
| c 26 | 16 | 80.0 | 688 | 7 | CO203373 |
| c 27 | 16 | 80.0 | 725 | 5 | BW014949 |
| 28 | 16 | 80.0 | 776 | 7 | CO983335 |
| 29 | 16 | 80.0 | 803 | 4 | BI825116 |
| c 30 | 16 | 80.0 | 810 | 9 | CG067730 |
| 31 | 16 | 80.0 | 896 | 4 | BF978318 |
| 32 | 16 | 80.0 | 970 | 9 | AG118710 |
| 33 | 16 | 80.0 | 1118 | 7 | CK208312 |
| 34 | 15.6 | 78.0 | 347 | 5 | BX548735 |
| 35 | 15.6 | 78.0 | 367 | 8 | AZ142355 |
| 36 | 15.6 | 78.0 | 526 | 4 | BU650234 |
| c 37 | 15.6 | 78.0 | 530 | 1 | AV714335 |
| c 38 | 15.6 | 78.0 | 624 | 8 | BH463715 |
| 39 | 15.6 | 78.0 | 653 | 9 | CR3339872 |
| 40 | 15.6 | 78.0 | 762 | 8 | BZ570281 |
| 41 | 15.6 | 78.0 | 824 | 2 | BF248110 |
| c 42 | 15.6 | 78.0 | 830 | 9 | CG893568 |
| 43 | 15.6 | 78.0 | 892 | 2 | BF028251 |
| c 44 | 15.6 | 78.0 | 1015 | 8 | BH656450 |
| c 45 | 15.4 | 77.0 | 242 | 6 | CB040958 |
| c 46 | 15.4 | 77.0 | 400 | 5 | BP665167 |
| c 47 | 15.4 | 77.0 | 448 | 5 | BP583126 |
| c 48 | 15.4 | 77.0 | 499 | 7 | CO278219 |
| c 49 | 15.4 | 77.0 | 520 | 7 | CO321105 |
| c 50 | 15.4 | 77.0 | 555 | 5 | BW029423 |

ALIGNMENTS

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| RESULT 1 | BG859034 | 636 bp | mRNA | linear | EST 29-MAY-2001 |
| LOCUS | 1024061A05.y1 | C. reinhardtii | CC-1690 | normalized | Lambda Zap II |
| DEFINITION | Chlamydomonas reinhardtii cDNA, mRNA sequence. | | | | |
| ACCESSION | BG859034 | | | | |
| VERSION | BG859034.1 | GI:14240218 | | | |
| KEYWORDS | EST. | | | | |
| SOURCE | Chlamydomonas reinhardtii | | | | |
| ORGANISM | Chlamydomonas reinhardtii | | | | |
| REFERENCE | 1 (bases 1 to 636) | | | | |
| AUTHORS | Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R. | | | | |
| TITLE | Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2 | | | | |
| JOURNAL | Unpublished (2000) | | | | |
| COMMENT | Contact: Charles Hauser DCMB Box 91000 Duke University Durham, NC 27708-1000 Tel.: 919 613 8159 Fax: 919 613 8177 Email: chauser@duke.edu. | | | | |
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| | /mol_type="mRNA" | | | | |
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 157.531 Seconds

(without alignments)
6151.841 Million cell updates/sec

Title: US-10-088-117A-21

Perfect score: 20

Sequence: 1 ggyvrtaccabscvcttc 20

Scoring table: IDENTITY_NUC

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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

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3: gb_in.*
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10: gb_ro.*
11: gb_ets.*
12: gb_gy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 16.4 | 82.0 | 100 | 6 | AX997781 |
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| 5 | 16.4 | 82.0 | 2486 | 6 | AX098605 |
| 6 | 16.4 | 82.0 | 2487 | 6 | AX098604 |
| 7 | 16.4 | 82.0 | 2487 | 6 | AX098606 |
| 8 | 16.4 | 82.0 | 2490 | 1 | SPU5974 |
| 9 | 16.4 | 82.0 | 2540 | 1 | RCDSMTORG |
| 10 | 16.4 | 82.0 | 2544 | 6 | AX098612 |
| 11 | 16.4 | 82.0 | 3211 | 1 | ECOCBPA |
| 12 | 16.4 | 82.0 | 4680 | 1 | ECTOR |
| 13 | 16.4 | 82.0 | 5637 | 1 | RCV49506 |
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| 15 | 16.4 | 82.0 | 6915 | 1 | SMA6085 |
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| c 23 | 16.4 | 82.0 | 18252 | 1 | D90737 | D90737 Escherichia |
| c 24 | 16.4 | 82.0 | 19650 | 1 | D90736 | D90736 Escherichia |
| c 25 | 16.4 | 82.0 | 22418 | 1 | AE008878 | AE008878 Salmonell |
| c 26 | 16.4 | 82.0 | 25409 | 1 | AE008741 | AE008741 Salmonell |
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| c 32 | 16.4 | 82.0 | 245050 | 1 | AL627280 | AL627280 Salmonell |
| c 33 | 16.4 | 82.0 | 250950 | 1 | AP005335 | AP005335 Vibrio vu |
| c 34 | 16.4 | 82.0 | 292504 | 1 | AE016981 | AE016981 Shigella |
| c 35 | 16.4 | 82.0 | 294050 | 1 | AL627268 | AL627268 Salmonell |
| c 36 | 16.4 | 82.0 | 297816 | 1 | AP002553 | AP002553 Escherich |
| c 37 | 16.4 | 82.0 | 299130 | 1 | AP005077 | AP005077 Vibrio pa |
| c 38 | 16.4 | 82.0 | 300592 | 1 | AE016846 | AE016846 Salmonell |
| c 39 | 16.4 | 82.0 | 301276 | 1 | AE016758 | AE016758 Escherich |
| c 40 | 16.4 | 82.0 | 301983 | 1 | AE016840 | AE016840 Salmonell |
| c 41 | 16.4 | 82.0 | 304490 | 1 | AE016806 | AE016806 Vibrio vu |
| c 42 | 16.4 | 82.0 | 349080 | 1 | CR378667 | CR378667 Photobact |
| c 43 | 15.6 | 78.0 | 110000 | 1 | AE016827_05 | Continuation (6 of |
| c 44 | 15.6 | 78.0 | 300540 | 1 | AE017154 | AE017154 Haemophil |
| c 45 | 15.6 | 78.0 | 314150 | 1 | CJ11168X1 | AL339074 Campyloba |
| c 46 | 15.6 | 78.0 | 348672 | 1 | CR378670 | CR378670 Photobact |
| c 47 | 15.4 | 77.0 | 1641 | 6 | BD269438 | BD269438 Mitomycin |
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ALIGNMENTS

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| RESULT 1 | AX098624 | AX098624 | 20 bp | DNA | linear | PAT 02-APR-2001 |
| LOCUS | Sequence 21 from Patent WO0120030. | | | | | |
| DEFINITION | AX098624 | | | | | |
| ACCESSION | AX098624.1 | GI:13537885 | | | | |
| VERSION | | | | | | |
| KEYWORDS | synthetic construct | | | | | |
| SOURCE | synthetic construct | | | | | |
| ORGANISM | other sequences; artificial sequences. | | | | | |
| REFERENCE | 1 | | | | | |
| AUTHORS | Giordano, G., dos Santos, J.P. and Mejean, V. | | | | | |
| TITLE | Nucleotide sequences derived from genes coding for trimethylamine n-oxide reductase, uses thereof in particular for detecting bacteria | | | | | |
| JOURNAL | Patent: WO 0120030-A 21 22-MAR-2001; | | | | | |
| FEATURES | CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR) | | | | | |
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| Db | 1 GGVYCTACCAACVCCCTTC 20 | | | | | |
| | | | | | | |
| RESULT 2 | | | | | | |
| AX989852/c | | | | | | |
| LOCUS | AX989852 | 100 bp | DNA | linear | PAT 16-JAN-2004 | |

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 22:48:55 ; Search time 19.9769 Seconds
(without alignments)
5926.580 Million cell updates/sec

Title: US-10-088-117A-21

Perfect score: 20

Sequence: 1 ggyvrtaccabscvcttc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 16.4 | 82.0 | 20 | AAF79960 | AAF79960 PCR prime |
| 2 | 16.4 | 82.0 | 100 | ACD77968 | Acet77968 E. coli K |
| 3 | 16.4 | 82.0 | 100 | ACD70045 | Acet70045 E. coli K |
| 4 | 16.4 | 82.0 | 1338 | AA888390 | AA888390 DNA encod |
| 5 | 16.4 | 82.0 | 1887 | AAH19221 | AAH19221 Human sec |
| 6 | 16.4 | 82.0 | 2358 | ACA19185 | ACA19185 Prokaryot |
| 7 | 16.4 | 82.0 | 2358 | ADA46037 | ADA46037 Bacterial |
| 8 | 16.4 | 82.0 | 2413 | ACA49353 | ACA49353 Prokaryot |
| 9 | 16.4 | 82.0 | 2445 | ACA51180 | ACA51180 Prokaryot |
| 10 | 16.4 | 82.0 | 2445 | ACA51914 | ACA51914 Prokaryot |
| 11 | 16.4 | 82.0 | 2475 | AAF79948 | AAF79948 Nucleotid |
| 12 | 16.4 | 82.0 | 2486 | AAF79944 | AAF79944 Nucleotid |
| 13 | 16.4 | 82.0 | 2487 | AAF79945 | AAF79945 Nucleotid |
| 14 | 16.4 | 82.0 | 2487 | AAF79943 | AAF79943 Nucleotid |
| 15 | 16.4 | 82.0 | 2544 | AAF79949 | AAF79949 Nucleotid |
| 16 | 16.4 | 82.0 | 2547 | ADA46046 | ADA46046 Bacterial |
| 17 | 16.4 | 82.0 | 3712 | AAH19184 | AAH19184 Human sec |
| 18 | 16.4 | 82.0 | 11275 | AAH43717 | AAH43717 E. coli g |
| 19 | 16.4 | 82.0 | 110000 | AAF42063 | Continuation (7 of |
| 20 | 15.4 | 77.0 | 1641 | AAc55833 | AAc55833 S. lavend |

| | | | | | | |
|----|------|------|-------|----|----------|---------------------|
| 21 | 15.4 | 77.0 | 1641 | 10 | ADe10252 | Adel0252 S. lavend |
| 22 | 15.4 | 77.0 | 53500 | 3 | AAc55842 | AAc55842 Complete |
| 23 | 15.4 | 77.0 | 53500 | 10 | ADe10261 | Adel0261 S. lavend |
| 24 | 14.8 | 74.0 | 129 | 5 | ABa15064 | Abal5064 Human ner |
| 25 | 14.8 | 74.0 | 395 | 8 | ABx45119 | Abx45119 Bovine ES |
| 26 | 14.8 | 74.0 | 442 | 8 | ABx46058 | Abx46058 Bovine ES |
| 27 | 14.8 | 74.0 | 519 | 8 | ABz53408 | Abz53408 Aspergill |
| 28 | 14.8 | 74.0 | 804 | 5 | AA85095 | AA85095 DNA encod |
| 29 | 14.8 | 74.0 | 1176 | 5 | AA85036 | AA85036 DNA encod |
| 30 | 14.8 | 74.0 | 1597 | 13 | ADs48720 | Adsa48720 Bacterial |
| 31 | 14.8 | 74.0 | 1794 | 3 | AAa30256 | AAa30256 Rat parti |
| 32 | 14.8 | 74.0 | 1913 | 13 | ACN37272 | ACn37272 Tumour-as |
| 33 | 14.8 | 74.0 | 2268 | 8 | ACA31543 | ACA31543 Prokaryot |
| 34 | 14.8 | 74.0 | 2280 | 13 | ABD33563 | ABd33563 Human can |
| 35 | 14.8 | 74.0 | 2286 | 12 | ADi81563 | Adi81563 Rat strep |
| 36 | 14.8 | 74.0 | 2286 | 12 | ADi81575 | Adi81575 Rat vanil |
| 37 | 14.8 | 74.0 | 2289 | 12 | ADi81627 | Adi81627 Rat ion c |
| 38 | 14.8 | 74.0 | 2310 | 6 | AA894752 | AA894752 Human DNA |
| 39 | 14.8 | 74.0 | 2319 | 6 | ABz82575 | ABz82575 Human sec |
| 40 | 14.8 | 74.0 | 2436 | 8 | ACA35519 | ACA35519 Prokaryot |
| 41 | 14.8 | 74.0 | 2478 | 11 | ACH99175 | ACH99175 Klebsiell |
| 42 | 14.8 | 74.0 | 2523 | 4 | AAF79947 | Aaf79947 Nucleotid |
| 43 | 14.8 | 74.0 | 2597 | 6 | ABK70006 | ABk70006 cDNA enco |
| 44 | 14.8 | 74.0 | 2597 | 9 | ADA01359 | Ada01359 Human PRO |
| 45 | 14.8 | 74.0 | 2597 | 9 | ADA43788 | Ada43788 Human CDN |
| 46 | 14.8 | 74.0 | 2597 | 9 | ADA43556 | Ada43556 Human CDN |
| 47 | 14.8 | 74.0 | 2597 | 9 | ADA01231 | Ada01231 Human PRO |
| 48 | 14.8 | 74.0 | 2597 | 9 | ADA01115 | Ada01115 Human CDN |
| 49 | 14.8 | 74.0 | 2597 | 9 | ADA43672 | Ada43672 Human CDN |
| 50 | 14.8 | 74.0 | 2597 | 9 | ADA06934 | Ada06934 Human PRO |

ALIGNMENTS

RESULT 1
AAF79960

ID AAF79960 standard; DNA; 20 BP.

AC AAF79960;

DT 11-JUN-2001 (first entry)

DE PCR primer used to amplify trimethylamine N-oxide reductase genes.

KW torA Gene; trimethylamine N-oxide reductase; flesh degradation;

KW spoilage bacteria; fish; crustacean; PCR primer; ss.

XX Synthetic.

XX WO200120030-A2.

XX 22-MAR-2001.

XX 15-SEP-2000; 2000WO-FR002578.

XX 15-SEP-1999; 99FR-00011543.

XX (CNRS) CENT NAT RECH SCI.

XX Giordano G, Dos Santos J, Mejean V;

XX WPI; 2001-244822/25.

PT Detecting bacteria that cause flesh degradation in fish, for testing

PT freshness, comprises using probes or primers based on the trimethylamine

XX N-oxide reductase system.

XX Claim 7; Page 42; 91pp; French.

XX PCR primers AAF79951-66 represent PCR primers used to amplify torA and

XX torC genes. TorA and torC are bacterial proteins of the trimethylamine N-

XX oxide reductase system. TorA nucleic acids are used for detecting, in a

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 08:20:11 ; Search time 6.17692 Seconds
(without alignments)
5298.032 Million cell updates/sec

Title: US-10-088-117A-21

Perfect score: 20

Sequence: 1 ggyvrtaccabscvcttc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents NA:*

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2: /cgm2_6/ptodata/1/ina/5B COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 16.4 | 82.0 | 1830121 | 4 | US-09-643-990A-1 |
| 3 | 15.4 | 77.0 | 1641 | 4 | US-09-266-965-67 |
| 4 | 15.4 | 77.0 | 53500 | 4 | US-09-266-965-76 |
| 5 | 14.8 | 74.0 | 2478 | 4 | US-09-489-039A-4970 |
| 6 | 14.8 | 74.0 | 2736 | 3 | US-09-235-451-3 |
| 7 | 14.8 | 74.0 | 2736 | 4 | US-09-978-303-3 |
| 8 | 14.4 | 72.0 | 654 | 4 | US-09-891-641-72 |
| 9 | 14.4 | 72.0 | 1305 | 4 | US-09-902-540-6383 |
| 10 | 14.4 | 72.0 | 2492 | 4 | US-09-902-540-421 |
| 11 | 14.4 | 72.0 | 128516 | 4 | US-09-949-016-13501 |
| 12 | 14.4 | 72.0 | 133157 | 4 | US-09-949-016-12541 |
| 13 | 14.2 | 71.0 | 3343 | 4 | US-09-503-890-1 |
| 14 | 14 | 70.0 | 307 | 4 | US-09-621-976-11201 |
| 15 | 14 | 70.0 | 601 | 4 | US-09-949-016-67294 |
| 16 | 14 | 70.0 | 2451 | 4 | US-09-543-681A-427 |
| 17 | 14 | 70.0 | 3425 | 4 | US-09-800-971-1 |
| 18 | 14 | 70.0 | 13953 | 3 | US-09-738-884-3 |
| 19 | 14 | 70.0 | 13953 | 4 | US-10-096-961A-3 |
| 20 | 14 | 70.0 | 36307 | 4 | US-09-949-016-17372 |
| 21 | 14 | 70.0 | 100463 | 4 | US-09-949-016-12511 |
| 22 | 14 | 70.0 | 100468 | 4 | US-09-949-016-13725 |
| 23 | 14 | 70.0 | 189560 | 4 | US-09-949-016-17202 |
| 24 | 13.8 | 69.0 | 219 | 4 | US-09-489-039A-7065 |
| 25 | 13.8 | 69.0 | 601 | 4 | US-09-949-016-135221 |
| 26 | 13.8 | 69.0 | 601 | 4 | US-09-949-016-170678 |
| 27 | 13.8 | 69.0 | 647 | 4 | US-09-777-430C-72 |

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|----|------|------|-------|---|---------------------|--------------------|
| 28 | 13.8 | 69.0 | 661 | 4 | US-09-814-915A-104 | Sequence 104, Appl |
| 29 | 13.8 | 69.0 | 725 | 4 | US-09-591-992-3 | Sequence 3, Appli |
| 30 | 13.8 | 69.0 | 725 | 4 | US-09-023-655-1344 | Sequence 1344, Ap |
| 31 | 13.8 | 69.0 | 741 | 3 | US-07-927-391-25 | Sequence 25, Appl |
| 32 | 13.8 | 69.0 | 741 | 4 | US-09-023-655-1165 | Sequence 1165, Ap |
| 33 | 13.8 | 69.0 | 752 | 6 | 5212073-1 | Patent No. 5212073 |
| 34 | 13.8 | 69.0 | 752 | 6 | 5212073-1 | Patent No. 5212073 |
| 35 | 13.8 | 69.0 | 772 | 4 | US-08-437-306-1 | Sequence 1, Appli |
| 36 | 13.8 | 69.0 | 849 | 4 | US-09-902-540-6085 | Sequence 6085, Ap |
| 37 | 13.8 | 69.0 | 1555 | 4 | US-09-902-540-267 | Sequence 267, App |
| 38 | 13.8 | 69.0 | 1712 | 4 | US-09-148-545-106 | Sequence 106, App |
| 39 | 13.8 | 69.0 | 1822 | 4 | US-09-148-545-105 | Sequence 105, App |
| 40 | 13.8 | 69.0 | 2417 | 4 | US-09-216-393B-306 | Sequence 306, App |
| 41 | 13.8 | 69.0 | 2417 | 4 | US-09-216-393B-308 | Sequence 308, App |
| 42 | 13.8 | 69.0 | 6060 | 4 | US-08-956-171E-534 | Sequence 534, App |
| 43 | 13.8 | 69.0 | 6060 | 4 | US-08-781-98A-534 | Sequence 534, App |
| 44 | 13.8 | 69.0 | 10903 | 4 | US-09-949-016-15530 | Sequence 15530, A |
| 45 | 13.8 | 69.0 | 15575 | 4 | US-09-949-016-12634 | Sequence 12634, A |
| 46 | 13.8 | 69.0 | 15575 | 4 | US-09-949-016-16568 | Sequence 16568, A |
| 47 | 13.8 | 69.0 | 33529 | 3 | US-09-144-085-3 | Sequence 3, Appli |
| 48 | 13.8 | 69.0 | 42376 | 4 | US-09-949-016-16276 | Sequence 16276, A |
| 49 | 13.8 | 69.0 | 48974 | 3 | US-08-920-422-17 | Sequence 17, Appl |
| 50 | 13.8 | 69.0 | 50797 | 4 | US-09-949-016-16346 | Sequence 16346, A |

ALIGNMENTS

RESULT 1

US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581

; GENERAL INFORMATION:

; APPLICANT: Fleischmann et al.

; TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3 1/2 inch diskette

; COMPUTER: Dell Pentium

; OPERATING SYSTEM: MS DOS v6.22

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/557,884

; FILING DATE: 25-Apr-2000

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/476,102

; FILING DATE: JUN-5-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Michelle S. Marks

; REGISTRATION NUMBER: 41,971

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1830121 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:25:53 ; Search time 21.2846 Seconds
(without alignments)
5776.400 Million cell updates/sec

Title: US-10-088-117A-21

Perfect score: 20

Sequence: 1 ggyvrtaccabscvcttc 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

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Published Applications NA:**
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6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 2 | 16.4 | 82.0 | 348 | 17 | US-10-335-977-1904 |
| C 3 | 16.4 | 82.0 | 2358 | 17 | US-10-369-493-24467 |
| C 4 | 16.4 | 82.0 | 2358 | 17 | US-10-369-493-24467 |
| C 5 | 16.4 | 82.0 | 2413 | 17 | US-10-282-122A-7055 |
| C 6 | 16.4 | 82.0 | 2445 | 17 | US-10-282-122A-37223 |
| C 7 | 16.4 | 82.0 | 2445 | 17 | US-10-282-122A-39050 |
| C 8 | 16.4 | 82.0 | 2547 | 17 | US-10-282-122A-39784 |
| C 9 | 16.4 | 82.0 | 11275 | 16 | US-10-369-493-24476 |
| C 10 | 16.4 | 82.0 | 1830121 | 17 | US-10-240-689-39 |
| C 11 | 16.4 | 82.0 | 1830121 | 18 | US-10-329-670-1 |
| C 12 | 16.4 | 82.0 | 1830121 | 18 | US-10-158-865-1 |

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|------|------|------|-------|----|----------------------|--------------------|
| 12 | 15.4 | 77.0 | 1641 | 10 | US-09-953-348-67 | Sequence 67, Appl |
| 13 | 15.4 | 77.0 | 1641 | 15 | US-10-267-255-67 | Sequence 76, Appl |
| 14 | 15.4 | 77.0 | 53500 | 10 | US-09-953-348-76 | Sequence 76, Appl |
| 15 | 15.4 | 77.0 | 53500 | 15 | US-10-267-255-76 | Sequence 76, Appl |
| C 16 | 14.8 | 74.0 | 201 | 18 | US-10-741-601-14846 | Sequence 14846, A |
| C 17 | 14.8 | 74.0 | 201 | 19 | US-10-741-600-37881 | Sequence 37881, A |
| C 18 | 14.8 | 74.0 | 376 | 18 | US-10-425-115-45319 | Sequence 45319, A |
| C 19 | 14.8 | 74.0 | 395 | 9 | US-09-960-352-10284 | Sequence 10284, A |
| C 20 | 14.8 | 74.0 | 442 | 9 | US-09-960-352-11223 | Sequence 11223, A |
| C 21 | 14.8 | 74.0 | 517 | 13 | US-10-027-632-129865 | Sequence 129865, A |
| C 22 | 14.8 | 74.0 | 517 | 17 | US-10-027-632-129865 | Sequence 129865, A |
| C 23 | 14.8 | 74.0 | 656 | 17 | US-10-424-599-26875 | Sequence 26875, A |
| C 24 | 14.8 | 74.0 | 719 | 13 | US-10-027-632-26627 | Sequence 26627, A |
| C 25 | 14.8 | 74.0 | 719 | 17 | US-10-027-632-26627 | Sequence 26627, A |
| C 26 | 14.8 | 74.0 | 769 | 13 | US-10-027-632-15109 | Sequence 15109, A |
| C 27 | 14.8 | 74.0 | 769 | 17 | US-10-027-632-15109 | Sequence 15109, A |
| C 28 | 14.8 | 74.0 | 804 | 18 | US-10-437-963-94508 | Sequence 94508, A |
| C 29 | 14.8 | 74.0 | 1541 | 17 | US-10-425-114-15108 | Sequence 15108, A |
| C 30 | 14.8 | 74.0 | 1597 | 17 | US-10-369-493-27150 | Sequence 27150, A |
| C 31 | 14.8 | 74.0 | 1615 | 17 | US-10-424-599-26876 | Sequence 26876, A |
| C 32 | 14.8 | 74.0 | 1937 | 19 | US-10-887-553A-387 | Sequence 387, App |
| C 33 | 14.8 | 74.0 | 2268 | 17 | US-10-282-122A-19413 | Sequence 19413, A |
| C 34 | 14.8 | 74.0 | 2280 | 18 | US-10-322-281-765 | Sequence 765, App |
| C 35 | 14.8 | 74.0 | 2286 | 17 | US-10-342-844-33 | Sequence 33, Appl |
| C 36 | 14.8 | 74.0 | 2286 | 17 | US-10-342-844-45 | Sequence 45, Appl |
| C 37 | 14.8 | 74.0 | 2289 | 17 | US-10-342-844-97 | Sequence 97, Appl |
| C 38 | 14.8 | 74.0 | 2310 | 16 | US-10-240-965-7 | Sequence 7, Appl |
| C 39 | 14.8 | 74.0 | 2436 | 17 | US-10-282-122A-23389 | Sequence 23389, A |
| C 40 | 14.8 | 74.0 | 2597 | 14 | US-10-245-752-91 | Sequence 91, Appl |
| C 41 | 14.8 | 74.0 | 2597 | 14 | US-10-245-859-91 | Sequence 91, Appl |
| C 42 | 14.8 | 74.0 | 2597 | 14 | US-10-245-103-91 | Sequence 91, Appl |
| C 43 | 14.8 | 74.0 | 2597 | 14 | US-10-245-107-91 | Sequence 91, Appl |
| C 44 | 14.8 | 74.0 | 2597 | 14 | US-10-245-143-91 | Sequence 91, Appl |
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| C 46 | 14.8 | 74.0 | 2597 | 14 | US-10-245-851-91 | Sequence 91, Appl |
| C 47 | 14.8 | 74.0 | 2597 | 14 | US-10-245-883-91 | Sequence 91, Appl |
| C 48 | 14.8 | 74.0 | 2597 | 14 | US-10-237-535-91 | Sequence 91, Appl |
| C 49 | 14.8 | 74.0 | 2597 | 14 | US-10-238-183-91 | Sequence 91, Appl |
| C 50 | 14.8 | 74.0 | 2597 | 14 | US-10-238-283-91 | Sequence 91, Appl |

ALIGNMENTS

RESULT 1
US-10-335-977-1903/c
; Sequence 1903, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-Dec-1997
; ATTORNEY/AGENT INFORMATION:

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 07:12:26 ; Search time 134.492 Seconds
(without alignments)
5660.438 Million cell updates/sec

Title: US-10-088-117A-21

Perfect score: 20

Sequence: 1 ggyvcrtaccabscvcttc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

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2: gb_est2.*

3: gb_hcc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_g881.*

9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 16.4 | 82.0 | 700 | 1 | AL509140 |
| 2 | 16.4 | 82.0 | 769 | 9 | CL671648 |
| 3 | 16.4 | 82.0 | 786 | 9 | CL666247 |
| 4 | 16.4 | 82.0 | 847 | 9 | CL670484 |
| 5 | 15.6 | 78.0 | 362 | 6 | BY667438 |
| 6 | 15.6 | 78.0 | 434 | 5 | BY461297 |
| 7 | 15.6 | 78.0 | 613 | 2 | BB651761 |
| 8 | 15.4 | 77.0 | 214 | 2 | BB216706 |
| 9 | 15.4 | 77.0 | 452 | 7 | CK326609 |
| 10 | 15.4 | 77.0 | 504 | 9 | CE239112 |
| 11 | 15.4 | 77.0 | 756 | 9 | AG593385 |
| 12 | 15.4 | 77.0 | 853 | 6 | CD751046 |
| 13 | 15.4 | 77.0 | 877 | 2 | BF623577 |
| 14 | 15.4 | 77.0 | 953 | 7 | CF455917 |
| 15 | 15.4 | 77.0 | 1070 | 7 | CF455948 |
| 16 | 15.4 | 77.0 | 1083 | 5 | BQ881573 |
| 17 | 15.4 | 77.0 | 1115 | 4 | BG477774 |
| 18 | 15.2 | 76.0 | 296 | 2 | BF551618 |
| 19 | 15.2 | 76.0 | 432 | 9 | CL214740 |
| 20 | 15.2 | 76.0 | 583 | 5 | BU702144 |
| 21 | 15.2 | 76.0 | 599 | 7 | CF892278 |
| 22 | 15.2 | 76.0 | 608 | 9 | CC875829 |
| 23 | 15.2 | 76.0 | 624 | 7 | CF727912 |
| 24 | 15.2 | 76.0 | 626 | 7 | CF894749 |

| | | | | | | | |
|---|----|------|------|------|---|----------|-----------|
| C | 25 | 15.2 | 76.0 | 667 | 7 | CN702732 | E0465H10- |
| | 26 | 15.2 | 76.0 | 676 | 7 | CF741585 | UI-M-HB0- |
| | 27 | 15.2 | 76.0 | 682 | 7 | CO429861 | UI-M-HX0- |
| C | 28 | 15.2 | 76.0 | 695 | 6 | CA242359 | SCEPFL308 |
| | 29 | 15.2 | 76.0 | 695 | 6 | CE362742 | tigr-g88- |
| | 30 | 15.2 | 76.0 | 712 | 5 | EX083115 | EX083115 |
| | 31 | 15.2 | 76.0 | 727 | 7 | CK634748 | UI-M-HD0- |
| | 32 | 15.2 | 76.0 | 732 | 7 | CF729144 | UI-M-HD0- |
| | 33 | 15.2 | 76.0 | 737 | 6 | CA511803 | UI-R-FJ0- |
| | 34 | 15.2 | 76.0 | 776 | 7 | CK635827 | UI-M-HN0- |
| C | 35 | 15.2 | 76.0 | 784 | 9 | AG275475 | Cyanidios |
| | 36 | 15.2 | 76.0 | 895 | 4 | BI952340 | HVSMEM000 |
| C | 37 | 15.2 | 76.0 | 1263 | 5 | BU588111 | AGENCOURT |
| | 38 | 15.2 | 76.0 | 2095 | 2 | BF302952 | 602030852 |
| | 39 | 15.2 | 76.0 | 4479 | 3 | AK049209 | Mus muscu |
| C | 40 | 14.8 | 74.0 | 184 | 1 | AI715375 | UI-R-Y0-a |
| | 41 | 14.8 | 74.0 | 184 | 5 | BQ303624 | QV2-BT063 |
| | 42 | 14.8 | 74.0 | 194 | 8 | BZ694126 | SP-Ba004 |
| | 43 | 14.8 | 74.0 | 211 | 2 | BE486215 | 174013 BA |
| | 44 | 14.8 | 74.0 | 235 | 7 | CV325892 | CM4-MT023 |
| C | 45 | 14.8 | 74.0 | 239 | 5 | EX633989 | EX633989 |
| | 46 | 14.8 | 74.0 | 257 | 2 | AW417197 | 53302 MAR |
| C | 47 | 14.8 | 74.0 | 258 | 1 | AA321284 | EST23748 |
| | 48 | 14.8 | 74.0 | 300 | 2 | BE401766 | CNW02EL08 |
| C | 49 | 14.8 | 74.0 | 313 | 8 | BZ943315 | CH240 81K |
| | 50 | 14.8 | 74.0 | 335 | 6 | CB108935 | K-EST0149 |

ALIGNMENTS

| | | | | |
|--------------------------------|---|--|--------|-----------------|
| AL509140 | 700 bp | mRNA | linear | EST 04-JAN-2001 |
| AL509140 | Hordeum vulgare | Barke developing caryopsis (3.-15.DAP) | | |
| Hordeum vulgare subsp. vulgare | cdna clone HY10N07V 5', mRNA | | | |
| sequence. | | | | |
| AL509140 | GI:12035643 | | | |
| VERSION | | | | |
| KEYWORDS | EST | | | |
| SOURCE | Hordeum vulgare subsp. vulgare | | | |
| ORGANISM | Hordeum vulgare subsp. vulgare | | | |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum. | | | |
| REFERENCE | 1 (bases 1 to 700) | | | |
| AUTHORS | Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A. | | | |
| TITLE | EST sequencing and analysis in barley | | | |
| JOURNAL | Unpublished (2000) | | | |
| COMMENT | Contact: Michalek W Institute for Plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de Seq primer: T3 primer for 5' end. | | | |
| FEATURES | Location/Qualifiers | | | |
| source | 1..700 | | | |
| | /organism="Hordeum vulgare subsp. vulgare" | | | |
| | /mol_type="mRNA" | | | |
| | /cultivar="barke" | | | |
| | /sub_species="vulgare" | | | |
| | /db_xref="taxon:112509" | | | |
| | /clone="HY10N07V" | | | |
| | /tissue_type="developing caryopsis (3.-15.DAP)" | | | |
| | /lab_host="XL0LR" | | | |
| | /clone_lib="Hordeum vulgare Barke developing caryopsis (3.-15.DAP)" | | | |
| | (3.-15.DAP)" | | | |
| | /note="Vector: plasmid pBK-CMV; Site 1: EcoRI; Site 2: XhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb | | | |

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 157.531 Seconds
(without alignments)
6151.841 Million cell updates/sec

Title: US-10-088-117A-22

Perfect score: 20

Sequence: 1 atcarrccnswvgcggtgcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 16.6 | 83.0 | 20 | 6 | AX098625 Sequence |
| 2 | 16.6 | 83.0 | 2292 | 1 | RSU25037 |
| 3 | 16.6 | 83.0 | 2475 | 6 | AX098610 Sequence |
| 4 | 16.6 | 83.0 | 2486 | 6 | AX098605 Sequence |
| 5 | 16.6 | 83.0 | 2487 | 6 | AX098604 Sequence |
| 6 | 16.6 | 83.0 | 2487 | 6 | AX098606 Sequence |
| 7 | 16.6 | 83.0 | 2490 | 1 | SFU5974 |
| 8 | 16.6 | 83.0 | 2523 | 6 | AX098609 Sequence |
| 9 | 16.6 | 83.0 | 2540 | 1 | RCDSYNOG |
| 10 | 16.6 | 83.0 | 2544 | 6 | AX098612 Sequence |
| 11 | 16.6 | 83.0 | 2750 | 1 | RCADSR |
| 12 | 16.6 | 83.0 | 3316 | 1 | RCADMS |
| 13 | 16.6 | 83.0 | 4680 | 1 | ECTOR |
| 14 | 16.6 | 83.0 | 5637 | 1 | RCU49506 |
| 15 | 16.6 | 83.0 | 6915 | 1 | SMA6085 |
| 16 | 16.6 | 83.0 | 7990 | 1 | AF016236 |
| 17 | 16.6 | 83.0 | 10726 | 1 | AE015567 |
| 18 | 16.6 | 83.0 | 11289 | 1 | AE005293 |
| 19 | 16.6 | 83.0 | 13067 | 1 | AE015128 |

| | | | | | |
|------|------|------|--------|----|-----------|
| c 20 | 16.6 | 83.0 | 18252 | 1 | D9Q737 |
| c 21 | 16.6 | 83.0 | 19650 | 1 | D90736 |
| c 22 | 16.6 | 83.0 | 110000 | 1 | U00096.10 |
| c 23 | 16.6 | 83.0 | 214911 | 2 | AC010537 |
| c 24 | 16.6 | 83.0 | 292504 | 1 | AE016981 |
| c 25 | 16.6 | 83.0 | 301276 | 1 | AE016758 |
| c 26 | 16.6 | 83.0 | 302650 | 1 | AP005958 |
| c 27 | 16.6 | 83.0 | 327773 | 1 | AP002554 |
| c 28 | 15.8 | 79.0 | 477 | 6 | AX098613 |
| c 29 | 15.8 | 79.0 | 22418 | 1 | AE008878 |
| c 30 | 15.8 | 79.0 | 56593 | 9 | AL445215 |
| c 31 | 15.8 | 79.0 | 245050 | 1 | AL627280 |
| c 32 | 15.8 | 79.0 | 300592 | 1 | AE016846 |
| c 33 | 15.6 | 78.0 | 201 | 11 | BV200860 |
| c 34 | 15.6 | 78.0 | 201 | 11 | BV200998 |
| c 35 | 15.6 | 78.0 | 303 | 6 | BD135671 |
| c 36 | 15.6 | 78.0 | 376 | 6 | AX321171 |
| c 37 | 15.6 | 78.0 | 411 | 6 | BD180449 |
| c 38 | 15.6 | 78.0 | 414 | 1 | AB107688 |
| c 39 | 15.6 | 78.0 | 445 | 6 | AX885383 |
| c 40 | 15.6 | 78.0 | 445 | 6 | BD024993 |
| c 41 | 15.6 | 78.0 | 459 | 9 | BT007045 |
| c 42 | 15.6 | 78.0 | 459 | 9 | CR541718 |
| c 43 | 15.6 | 78.0 | 459 | 12 | AX335665 |
| c 44 | 15.6 | 78.0 | 459 | 12 | BT007776 |
| c 45 | 15.6 | 78.0 | 501 | 6 | AX321130 |
| c 46 | 15.6 | 78.0 | 501 | 6 | AX321420 |
| c 47 | 15.6 | 78.0 | 518 | 6 | AX381591 |
| c 48 | 15.6 | 78.0 | 599 | 6 | AX321189 |
| c 49 | 15.6 | 78.0 | 638 | 5 | AF043542 |
| c 50 | 15.6 | 78.0 | 647 | 6 | BD079935 |

ALIGNMENTS

RESULT 1
AX098625
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

AX098625
Sequence 22 from Patent WO0120030.
AX098625
AX098625.1 GI:13537886

synthetic construct
synthetic construct
other sequences; artificial sequences.

1
Giordano,G., dos Santos,J.P. and Mejean,V.

Nucleotide sequences derived from genes coding for trimethylamine
n-oxide reductase, uses thereof in particular for detecting
bacteria

Patent: WO 0120030-A 22 23-MAR-2001;

CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

Location/Qualifiers

1. 20

/organism="synthetic construct"

/mol type="unassigned DNA"

/db xref="taxon:32630"

/note="amorce PCR"

ORIGIN

Query Match 83.0%; Score 16.6; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCARRCCNSWVGCGTGC 20

Db 1 ATCARRCCNSWVGCGTGC 20

RESULT 2

RSU25037/c

LOCUS

RSU25037

2292 bp

DNA

linear

BCT 16-APR-1998

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 22:48:55 ; Search time 19,9769 Seconds
(without alignments)
5946.580 Million cell updates/sec

Title: US-10-088-117A-22

Perfect score: 20

Sequence: 1 atccaricnswggcggtgcc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 50 summaries

Database : N Geneseq 16Dec04:*

- 1: geneseqn1980a:*
- 2: geneseqn1990a:*
- 3: geneseqn2000a:*
- 4: geneseqn2001a:*
- 5: geneseqn2001b:*
- 6: geneseqn2002a:*
- 7: geneseqn2002b:*
- 8: geneseqn2003a:*
- 9: geneseqn2003b:*
- 10: geneseqn2003c:*
- 11: geneseqn2003d:*
- 12: geneseqn2004a:*
- 13: geneseqn2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 16.6 | 83.0 | 20 | 4 AAF79961 | AAF79961 PCR prime |
| C. 2 | 16.6 | 83.0 | 2475 | 4 AAF79948 | AAF79948 Nucleotid |
| C. 3 | 16.6 | 83.0 | 2486 | 4 AAF79944 | AAF79944 Nucleotid |
| C. 4 | 16.6 | 83.0 | 2487 | 4 AAF79945 | AAF79945 Nucleotid |
| C. 5 | 16.6 | 83.0 | 2487 | 4 AAF79943 | AAF79943 Nucleotid |
| C. 6 | 16.6 | 83.0 | 2523 | 4 AAF79947 | AAF79947 Nucleotid |
| C. 7 | 16.6 | 83.0 | 2544 | 4 AAF79949 | AAF79949 Nucleotid |
| C. 8 | 16.6 | 83.0 | 2547 | 13 ADS45046 | ADS45046 Bacterial |
| C. 9 | 16.6 | 83.0 | 2853 | 5 AAF79908 | AAF79908 DNA encod |
| C. 10 | 16.6 | 83.0 | 2853 | 5 AAF79906 | AAF79906 DNA encod |
| C. 11 | 16.6 | 83.0 | 2853 | 5 AAF79927 | AAF79927 DNA encod |
| C. 12 | 16.6 | 83.0 | 2853 | 5 AAF79945 | AAF79945 DNA encod |
| C. 13 | 16.6 | 83.0 | 11275 | 6 AAF79917 | AAF79917 E. coli g |
| C. 14 | 15.8 | 79.0 | 477 | 4 AAF79950 | AAF79950 Partial n |
| C. 15 | 15.6 | 78.0 | 303 | 6 AAF79945 | AAF79945 cDNA enco |
| C. 16 | 15.6 | 78.0 | 376 | 6 AAF79945 | AAF79945 cDNA enco |
| C. 17 | 15.6 | 78.0 | 376 | 6 AAF79945 | AAF79945 cDNA enco |
| C. 18 | 15.6 | 78.0 | 445 | 3 AAF79945 | AAF79945 Human sec |
| C. 19 | 15.6 | 78.0 | 501 | 6 AAF79945 | AAF79945 Lung smal |
| C. 20 | 15.6 | 78.0 | 518 | 6 AAF79945 | AAF79945 Human col |

| | | | | | |
|-------|------|------|------|-------------|--------------------|
| 21 | 15.6 | 78.0 | 576 | 13 ADS45929 | ADS45929 Bacterial |
| 22 | 15.6 | 78.0 | 599 | 6 AAF79961 | AAF79961 Lung smal |
| 23 | 15.6 | 78.0 | 647 | 2 AAF79945 | AAF79945 Gene enco |
| 24 | 15.6 | 78.0 | 670 | 3 AAF79945 | AAF79945 Human nm2 |
| 25 | 15.6 | 78.0 | 670 | 6 AAF79945 | AAF79945 cDNA enco |
| 26 | 15.6 | 78.0 | 670 | 6 AAF79945 | AAF79945 Human NM2 |
| 27 | 15.6 | 78.0 | 670 | 8 AAF79945 | AAF79945 Gene diff |
| 28 | 15.6 | 78.0 | 670 | 10 AAF79945 | AAF79945 Human chr |
| 29 | 15.6 | 78.0 | 670 | 12 AAF79945 | AAF79945 Human nm2 |
| 30 | 15.6 | 78.0 | 670 | 13 AAF79945 | AAF79945 Breast ca |
| 31 | 15.6 | 78.0 | 670 | 13 AAF79945 | AAF79945 Tumour-as |
| 32 | 15.6 | 78.0 | 670 | 13 AAF79945 | AAF79945 PRO polyp |
| 33 | 15.6 | 78.0 | 670 | 13 AAF79945 | AAF79945 Human pro |
| 34 | 15.6 | 78.0 | 670 | 13 AAF79945 | AAF79945 Human pro |
| 35 | 15.6 | 78.0 | 670 | 13 AAF79945 | AAF79945 Human pen |
| 36 | 15.6 | 78.0 | 670 | 13 AAF79945 | AAF79945 Human BCC |
| 37 | 15.6 | 78.0 | 670 | 13 AAF79945 | AAF79945 Human sof |
| 38 | 15.6 | 78.0 | 670 | 13 AAF79945 | AAF79945 Full leng |
| 39 | 15.6 | 78.0 | 670 | 13 AAF79945 | AAF79945 Mouse isc |
| C. 40 | 15.4 | 77.0 | 256 | 6 AAF79945 | AAF79945 Human ORF |
| C. 41 | 15 | 75.0 | 573 | 8 AAF79945 | AAF79945 Prokaryot |
| C. 42 | 15 | 75.0 | 1284 | 11 AAF79945 | AAF79945 Mouse mRN |
| C. 43 | 15 | 75.0 | 1431 | 3 AAF79945 | AAF79945 HIV gp120 |
| C. 44 | 15 | 75.0 | 1437 | 3 AAF79945 | AAF79945 HIV gp120 |
| C. 45 | 15 | 75.0 | 1944 | 3 AAF79945 | AAF79945 HIV gp140 |
| C. 46 | 15 | 75.0 | 1950 | 3 AAF79945 | AAF79945 HIV gp140 |
| C. 47 | 15 | 75.0 | 2466 | 3 AAF79945 | AAF79945 HIV gp160 |
| C. 48 | 15 | 75.0 | 2493 | 3 AAF79945 | AAF79945 HIV gp160 |
| C. 49 | 15 | 75.0 | 2547 | 3 AAF79945 | AAF79945 HIV gp160 |
| C. 50 | 15 | 75.0 | 2550 | 6 AAF79945 | AAF79945 HIV-1 env |

ALIGNMENTS

RESULT 1

AAF79961 ID AAF79961 standard; DNA; 20 BP.

AC AAF79961;

DT 11-JUN-2001 (first entry)

DE PCR primer used to amplify trimethylamine N-oxide reductase genes.

KW torA gene; trimethylamine N-oxide reductase; flesh degradation;

XX spoilage bacteria; fish; crustacean; PCR primer; ss.

OS Synthetic.

FN WO200120030-A2.

PD 22-MAR-2001.

XX 15-SEP-2000; 2000WO-FR002578.

XX 15-SEP-1999; 99FR-00011543.

XX (CNRS) CENT NAT RECH SCI.

XX Giordano G, Dos Santos J, Mejean V;

XX WPI; 2001-244822/25.

XX Detecting bacteria that cause flesh degradation in fish, for testing

XX freshness, comprises using probes or primers based on the trimethylamine

XX N-oxide reductase system.

XX Claim 7; Page 42; 91pp; French.

XX PCR primers AAF79951-66 represent PCR primers used to amplify torA and

XX torC genes. TorA and torC are bacterial proteins of the trimethylamine N-

XX oxide reductase system. TorA nucleic acids are used for detecting, in a

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:25:53 ; Search time 21.2846 Seconds
(without alignments)
5776.400 Million cell updates/sec

Title: US-10-088-117A-22

Perfect score: 20

Sequence: 1 atcarrccnswvgcggtgcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Published Applications NA.*

| | |
|-----|--|
| 1: | /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.* |
| 2: | /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.* |
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| 4: | /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.* |
| 5: | /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.* |
| 6: | /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.* |
| 7: | /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.* |
| 8: | /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.* |
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| 10: | /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.* |
| 11: | /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.* |
| 12: | /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.* |
| 13: | /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.* |
| 14: | /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.* |
| 15: | /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.* |
| 16: | /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.* |
| 17: | /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.* |
| 18: | /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.* |
| 19: | /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.* |
| 20: | /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.* |
| 21: | /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.* |
| 22: | /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------------------|--------------------|
| C 1 | 16.6 | 83.0 | 2547 | 17 US-10-369-493-24476 | Sequence 24476, A |
| C 2 | 15.6 | 83.0 | 11275 | 16 US-10-240-689-39 | Sequence 39, Appl |
| C 3 | 15.6 | 78.0 | 376 | 9 US-09-833-790-188 | Sequence 188, Appl |
| 4 | 15.6 | 78.0 | 456 | 17 US-10-133-628-9 | Sequence 9, Appli |
| 5 | 15.6 | 78.0 | 456 | 17 US-10-133-628-10 | Sequence 10, Appl |
| 6 | 15.6 | 78.0 | 501 | 9 US-09-833-790-147 | Sequence 147, Appl |
| 7 | 15.6 | 78.0 | 501 | 9 US-09-833-790-437 | Sequence 437, Appl |
| 8 | 15.6 | 78.0 | 518 | 9 US-09-919-580-529 | Sequence 529, Appl |
| 9 | 15.6 | 78.0 | 576 | 17 US-10-369-493-24359 | Sequence 24359, A |
| 10 | 15.6 | 78.0 | 599 | 9 US-09-833-790-206 | Sequence 206, Appl |
| 11 | 15.6 | 78.0 | 670 | 15 US-10-171-581-32 | Sequence 32, Appl |

| | | | | | |
|------|------|------|----------|-------------------------|--------------------|
| 12 | 15.6 | 78.0 | 670 | 17 US-10-133-937-49 | Sequence 49, Appl |
| 13 | 15.6 | 78.0 | 670 | 17 US-10-172-118-780 | Sequence 780, Appl |
| 14 | 15.6 | 78.0 | 670 | 17 US-10-159-563-49 | Sequence 49, Appl |
| 15 | 15.6 | 78.0 | 670 | 17 US-10-440-464-89 | Sequence 89, Appl |
| 16 | 15.6 | 78.0 | 670 | 17 US-10-342-887-780 | Sequence 780, Appl |
| 17 | 15.6 | 78.0 | 5071 | 18 US-10-723-860-1220 | Sequence 1220, Ap |
| 18 | 15 | 75.0 | 393 | 15 US-10-156-761-3336 | Sequence 3336, Ap |
| 19 | 15 | 75.0 | 573 | 17 US-10-282-122A-27530 | Sequence 27530, A |
| C 20 | 15 | 75.0 | 974 | 18 US-10-425-115-121422 | Sequence 121422, A |
| C 21 | 15 | 75.0 | 1284 | 13 US-10-087-192-560 | Sequence 560, App |
| 22 | 15 | 75.0 | 1362 | 15 US-10-156-761-575 | Sequence 575, App |
| 23 | 15 | 75.0 | 1431 | 10 US-09-899-575-6 | Sequence 6, Appli |
| 24 | 15 | 75.0 | 1437 | 10 US-09-899-575-12 | Sequence 12, Appl |
| 25 | 15 | 75.0 | 1944 | 10 US-09-899-575-7 | Sequence 7, Appli |
| 26 | 15 | 75.0 | 1950 | 10 US-09-899-575-13 | Sequence 13, Appl |
| 27 | 15 | 75.0 | 2466 | 10 US-09-899-575-8 | Sequence 8, Appli |
| 28 | 15 | 75.0 | 2493 | 10 US-09-899-575-14 | Sequence 14, Appl |
| 29 | 15 | 75.0 | 2547 | 10 US-09-899-575-9 | Sequence 9, Appli |
| 30 | 15 | 75.0 | 2550 | 10 US-09-967-464-65 | Sequence 65, Appl |
| 31 | 15 | 75.0 | 2562 | 18 US-10-441-926-3 | Sequence 3, Appli |
| 32 | 15 | 75.0 | 2562 | 18 US-10-441-949-3 | Sequence 3, Appli |
| 33 | 15 | 75.0 | 2565 | 10 US-09-899-575-15 | Sequence 15, Appl |
| 34 | 15 | 75.0 | 2565 | 10 US-09-899-575-97 | Sequence 97, Appl |
| 35 | 15 | 75.0 | 2565 | 15 US-10-130-435-205 | Sequence 205, Appl |
| 36 | 15 | 75.0 | 2568 | 10 US-09-967-464-66 | Sequence 66, Appl |
| C 37 | 15 | 75.0 | 3720 | 17 US-10-282-122A-40445 | Sequence 40445, A |
| 38 | 15 | 75.0 | 32591 | 17 US-10-085-117-187 | Sequence 187, App |
| 39 | 15 | 75.0 | 90256608 | 18 US-10-470-565-1 | Sequence 1, Appli |
| 40 | 15 | 75.0 | 90256608 | 15 US-10-156-761-1 | Sequence 1, Appli |
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| 42 | 14.8 | 74.0 | 399 | 17 US-10-369-493-31975 | Sequence 641, App |
| 43 | 14.8 | 74.0 | 404 | 9 US-09-922-217-641 | Sequence 641, App |
| 44 | 14.8 | 74.0 | 404 | 9 US-09-833-263-641 | Sequence 641, App |
| 45 | 14.8 | 74.0 | 404 | 13 US-10-025-380-641 | Sequence 641, App |
| 46 | 14.8 | 74.0 | 612 | 18 US-10-363-829-100 | Sequence 100, App |
| 47 | 14.6 | 73.0 | 405 | 10 US-09-233-183A-2681 | Sequence 2681, Ap |
| 48 | 14.6 | 73.0 | 457 | 9 US-09-833-790-137 | Sequence 137, App |
| 49 | 14.6 | 73.0 | 886 | 18 US-10-425-115-91080 | Sequence 91080, A |
| 50 | 14.6 | 73.0 | 947 | 17 US-10-424-599-79483 | Sequence 79483, A |

ALIGNMENTS

RESULT 1
US-10-369-493-24476/c
; Sequence 24476, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 24476
; LENGTH: 2547
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-369-493-24476

Query Match 83.0%; Score 16.6; DB 17; Length 2547;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 14; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATCARRCCNWSVGGCGTGCC 20

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 07:12:26 ; Search time 134.492 Seconds
(without alignments)
5660.438 Million cell updates/sec

Title: US-10-088-117A-22

Perfect score: 20

Sequence: 1 atcarrcnswggcggtgcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

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4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| C 2 | 16.6 | 83.0 | 406 | 5 | BP094961 |
| C 3 | 16.6 | 83.0 | 543 | 2 | BE323149 |
| C 4 | 16.6 | 83.0 | 638 | 7 | CF864909 |
| C 5 | 15.8 | 79.0 | 501 | 7 | CK098963 |
| C 6 | 15.6 | 78.0 | 124 | 1 | AA471268 |
| C 7 | 15.6 | 78.0 | 138 | 6 | CD739260 |
| C 8 | 15.6 | 78.0 | 151 | 6 | CD615018 |
| C 9 | 15.6 | 78.0 | 161 | 6 | CD615025 |
| C 10 | 15.6 | 78.0 | 163 | 6 | CB119089 |
| C 11 | 15.6 | 78.0 | 164 | 6 | CD615026 |
| C 12 | 15.6 | 78.0 | 167 | 6 | CD615017 |
| C 13 | 15.6 | 78.0 | 171 | 6 | CD731078 |
| C 14 | 15.6 | 78.0 | 173 | 6 | CB119092 |
| C 15 | 15.6 | 78.0 | 179 | 4 | BM841467 |
| C 16 | 15.6 | 78.0 | 180 | 6 | CD615015 |
| C 17 | 15.6 | 78.0 | 180 | 6 | CD615016 |
| C 18 | 15.6 | 78.0 | 182 | 6 | CD615029 |
| C 19 | 15.6 | 78.0 | 183 | 6 | CD615030 |
| C 20 | 15.6 | 78.0 | 192 | 2 | BE775542 |
| C 21 | 15.6 | 78.0 | 208 | 6 | CD615022 |
| C 22 | 15.6 | 78.0 | 208 | 7 | D56165 |
| C 23 | 15.6 | 78.0 | 214 | 7 | CF644006 |
| C 24 | 15.6 | 78.0 | 221 | 6 | CB122740 |

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| 27 | 15.6 | 78.0 | 245 | 6 | CD615019 |
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| 33 | 15.6 | 78.0 | 268 | 7 | CN981851 |
| 34 | 15.6 | 78.0 | 273 | 2 | AW418176 |
| 35 | 15.6 | 78.0 | 279 | 6 | CB298002 |
| 36 | 15.6 | 78.0 | 285 | 6 | CB117146 |
| 37 | 15.6 | 78.0 | 285 | 7 | CF116418 |
| 38 | 15.6 | 78.0 | 297 | 2 | BE845901 |
| 39 | 15.6 | 78.0 | 300 | 1 | AU098718 |
| 40 | 15.6 | 78.0 | 302 | 2 | BE227297 |
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| 44 | 15.6 | 78.0 | 317 | 6 | CB113993 |
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| 47 | 15.6 | 78.0 | 326 | 7 | CN221996 |
| 48 | 15.6 | 78.0 | 330 | 7 | CK612075 |
| 49 | 15.6 | 78.0 | 334 | 7 | CV312969 |
| 50 | 15.6 | 78.0 | 335 | 7 | CN267145 |

ALIGNMENTS

RESULT 1
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LOCUS AV626231 Chlamydomonas reinhardtii 5' to 0.04% CO2 Chlamydomonas
DEFINITION reinhardtii cDNA clone LCL004907 r 5', mRNA sequence.
ACCESSION AV626231
VERSION AV626231.1 GI:10788511
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 244)
AUTHORS Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y. and Tabata,S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)
MEDLINE 20539644
PubMed 11089912
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 252-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
Location/Qualifiers
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/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="C9"
/db_xref="taxon:3055"
/clone="LCL004907 r"
/note="Vector: pBluescriptII SK-; Site 1: EcoRI; Site 2:
XhoI. The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"

ORIGIN

Query Match 83.0%; Score 16.6; DB 1; Length 244;
Best Local Similarity 70.0%; Pred. No. 5.1e+02;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 133.901 Seconds
(without alignments)
6151.841 Million cell updates/sec

Title: US-10-088-117A-23

Perfect score: 17

Sequence: 1 gbcactcdgtytgagg 17

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

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2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 14.2 | 83.5 | 377 | 6 | AX331490 Sequence |
| 3 | 14.2 | 83.5 | 506 | 8 | AB108334 Phleum pr |
| 4 | 14.2 | 83.5 | 586 | 6 | CQ780984 Sequence |
| 5 | 14.2 | 83.5 | 586 | 6 | BD125693 Primer fo |
| 6 | 14.2 | 83.5 | 738 | 3 | CAU94757 |
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| 9 | 14.2 | 83.5 | 813 | 9 | BC029416 Homo sapi |
| 10 | 14.2 | 83.5 | 1075 | 9 | BC020203 Homo sapi |
| 11 | 14.2 | 83.5 | 1559 | 9 | AF217989 Homo sapi |
| 12 | 14.2 | 83.5 | 2000 | 6 | BD270046 Secreted |
| 13 | 14.2 | 83.5 | 2146 | 5 | BC078093 Xenopus l |
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| 15 | 14.2 | 83.5 | 2238 | 9 | AY450874 Cercopit |
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| C 23 | 14.2 | 83.5 | 2443 | 9 | AY358477 Homo sapi |
| C 24 | 14.2 | 83.5 | 2447 | 6 | AX206905 Sequence |
| C 25 | 14.2 | 83.5 | 2475 | 6 | AX098610 Sequence |
| C 26 | 14.2 | 83.5 | 2486 | 6 | AX098605 Sequence |
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| C 35 | 14.2 | 83.5 | 2841 | 6 | AX106709 Sequence |
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| C 39 | 14.2 | 83.5 | 5006 | 10 | MMU24171 |
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| C 42 | 14.2 | 83.5 | 7990 | 1 | AF016236 Rhodobact |
| C 43 | 14.2 | 83.5 | 10726 | 1 | AE015567 Shewanell |
| C 44 | 14.2 | 83.5 | 11034 | 1 | AE004247 Vibrio ch |
| C 45 | 14.2 | 83.5 | 11289 | 1 | AE005293 Escherich |
| C 46 | 14.2 | 83.5 | 12083 | 1 | AE002012 Deinococc |
| C 47 | 14.2 | 83.5 | 13067 | 1 | AE015128 Shigella |
| C 48 | 14.2 | 83.5 | 18252 | 1 | D90737 Escherichia |
| C 49 | 14.2 | 83.5 | 19650 | 1 | D90736 Escherichia |
| C 50 | 14.2 | 83.5 | 31059 | 9 | AC009005 Homo sapi |
| | | | 38102 | 9 | AP001047 Homo sapi |

ALIGNMENTS

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| RESULT 1 | AX098626 | 17 bp | DNA | linear | PAT 02-APR-2001 |
| LOCUS | Sequence 23 from Patent WO0120030. | | | | |
| DEFINITION | AX098626 | | | | |
| ACCESSION | AX098626.1 | | | | |
| VERSION | GI:13537887 | | | | |
| KEYWORDS | synthetic construct | | | | |
| SOURCE | synthetic construct | | | | |
| ORGANISM | other sequences; artificial sequences. | | | | |
| REFERENCE | 1 | | | | |
| AUTHORS | Giordano, G., dos Santos, J.P. and Mejean, V. | | | | |
| TITLE | Nucleotide sequences derived from genes coding for trimethylamine n-oxide reductase, uses thereof in particular for detecting bacteria | | | | |
| JOURNAL | Patent: WO 0120030-A 23 22-MAR-2001; | | | | |
| FEATURES | CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR) | | | | |
| source | Location/Qualifiers | | | | |
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| | /db_xref="taxon:32630" | | | | |
| | /note="amorce PCR" | | | | |

ORIGIN

Query Match 83.5%; Score 14.2; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e+02; 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 GBCACRTCDGTYTGAG 17

Db 1 GBCACRTCDGTYTGAG 17

RESULT 2

AX331490

LOCUS

AX331490

377 bp

DNA

linear

PAT 09-JAN-2002

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 22:48:55 ; Search time 16.9804 Seconds
(without alignments)
5926.580 Million cell updates/sec

Title: US-10-088-117A-23
Perfect score: 17
Sequence: 1 gbcartcdgtygtggyg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
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2: Geneseqn1980s:*
3: Geneseqn1990s:*
4: Geneseqn2000s:*
5: Geneseqn2001as:*
6: Geneseqn2001bs:*
7: Geneseqn2002as:*
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9: Geneseqn2003as:*
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13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 14.2 | 83.5 | 223 | AAT21689 | Aat21689 Human gen |
| 3 | 14.2 | 83.5 | 377 | ABL63662 | ABL63662 Breast ca |
| 4 | 14.2 | 83.5 | 481 | ACH36846 | Ach36846 Human end |
| 5 | 14.2 | 83.5 | 488 | ACH34538 | Ach34538 Human end |
| 6 | 14.2 | 83.5 | 586 | AAK92664 | Aak92664 Human cdn |
| 7 | 14.2 | 83.5 | 586 | ADL29091 | Adl29091 3' end of |
| 8 | 14.2 | 83.5 | 812 | AAH87695 | Aah87695 Human sec |
| 9 | 14.2 | 83.5 | 812 | AAC939855 | Aac939855 Human sec |
| 10 | 14.2 | 83.5 | 1559 | AAS97017 | Aas97017 DNA encod |
| 11 | 14.2 | 83.5 | 1921 | AAH75108 | Aah75108 DNA encod |
| 12 | 14.2 | 83.5 | 2000 | AAa23430 | Aaa23430 CDNA enco |
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| c 24 | 14.2 | 83.5 | 2443 | 9 | ADA76007 | Ada76007 Human PRO |
| c 25 | 14.2 | 83.5 | 2443 | 9 | ADA18657 | Ada18657 Human PRO |
| c 26 | 14.2 | 83.5 | 2443 | 9 | ADA61280 | Ada61280 Homo sapi |
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| c 28 | 14.2 | 83.5 | 2443 | 9 | ADB27606 | ADB27606 cDNA enco |
| c 29 | 14.2 | 83.5 | 2443 | 9 | ADA86085 | Ada86085 Novel hum |
| c 30 | 14.2 | 83.5 | 2443 | 9 | ADA86085 | Ada86085 Novel hum |
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| c 32 | 14.2 | 83.5 | 2443 | 9 | ADA86085 | Ada86085 Novel hum |
| c 33 | 14.2 | 83.5 | 2443 | 9 | ADA86085 | Ada86085 Novel hum |
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| c 42 | 14.2 | 83.5 | 2443 | 9 | ADA86085 | Ada86085 Novel hum |
| c 43 | 14.2 | 83.5 | 2443 | 9 | ADA86085 | Ada86085 Novel hum |
| c 44 | 14.2 | 83.5 | 2443 | 9 | ADA86085 | Ada86085 Novel hum |
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| c 46 | 14.2 | 83.5 | 2443 | 9 | ADA86085 | Ada86085 Novel hum |
| c 47 | 14.2 | 83.5 | 2443 | 9 | ADA86085 | Ada86085 Novel hum |
| c 48 | 14.2 | 83.5 | 2443 | 9 | ADA86085 | Ada86085 Novel hum |
| c 49 | 14.2 | 83.5 | 2443 | 9 | ADA86085 | Ada86085 Novel hum |
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ALIGNMENTS

RESULT 1

AA79962 ID AAF79962 standard; DNA; 17 BP.

XX AC AAF79962;

XX DT 11-JUN-2001 (first entry)

XX DE PCR primer used to amplify trimethylamine N-oxide reductase genes.

XX KW torA gene; trimethylamine N-oxide reductase; flesh degradation;

XX KW spoilage bacteria; fish; crustacean; PCR primer; ss.

XX OS Synthetic.

XX FN WO200120030-A2.

XX PD 22-MAR-2001.

XX PF 15-SEP-2000; 2000WO-FR002578.

XX PR 15-SEP-1999; 99PR-00011543.

XX PA (CNRS) CENT NAT RECH SCI.

XX PI Giordano G, Dos Santos J, Mejean V;

XX DR WPI; 2001-244822/25.

XX PT Detecting bacteria that cause flesh degradation in fish, for testing
freshness, comprises using probes or primers based on the trimethylamine
N-oxide reductase system.

XX PS Claim 7; Page 42; 91pp; French.

XX CC PCR primers AAF79951-66 represent PCR primers used to amplify torA and
torC genes. TorA and torC are bacterial proteins of the trimethylamine N-
oxide reductase system. TorA nucleic acids are used for detecting, in a

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:25:53 ; Search time 18.0919 Seconds
(without alignments)
5776.400 Million cell updates/sec

Title: US-10-088-117A-23

Perfect score: 17

Sequence: 1 gbcactcdgtyr-gygg 17

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 25 | 14.2 | 83.5 | 2443 | 14 | US-10-121-050-57 | Sequence 57, Appl |
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| C 32 | 14.2 | 83.5 | 2443 | 14 | US-10-140-928-57 | Sequence 57, Appl |
| C 33 | 14.2 | 83.5 | 2443 | 14 | US-10-121-045-57 | Sequence 57, Appl |
| C 34 | 14.2 | 83.5 | 2443 | 14 | US-10-123-292-57 | Sequence 57, Appl |
| C 35 | 14.2 | 83.5 | 2443 | 14 | US-10-123-903-57 | Sequence 57, Appl |
| C 36 | 14.2 | 83.5 | 2443 | 14 | US-10-124-819-57 | Sequence 57, Appl |
| C 37 | 14.2 | 83.5 | 2443 | 14 | US-10-124-822-57 | Sequence 57, Appl |
| C 38 | 14.2 | 83.5 | 2443 | 14 | US-10-140-925-57 | Sequence 57, Appl |
| C 39 | 14.2 | 83.5 | 2443 | 14 | US-10-160-498-57 | Sequence 57, Appl |
| C 40 | 14.2 | 83.5 | 2443 | 14 | US-10-124-824-57 | Sequence 57, Appl |
| C 41 | 14.2 | 83.5 | 2443 | 14 | US-10-127-825A-57 | Sequence 57, Appl |
| C 42 | 14.2 | 83.5 | 2443 | 14 | US-10-127-829A-57 | Sequence 57, Appl |
| C 43 | 14.2 | 83.5 | 2443 | 14 | US-10-127-835A-57 | Sequence 57, Appl |
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ALIGNMENTS

RESULT 1
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; Sequence 932, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C;
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 932
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

GenCore version 5.1.6
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Run on: June 2, 2005, 07:12:26 ; Search time 114.318 Seconds
(without alignments)
5660.438 Million cell updates/sec

Title: US-10-088-117A-23

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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3: gb_hcc.*
4: gb_est3.*
5: gb_est4.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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VERSION C00843.1 GI:1433073
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 220)
AUTHORS Okubo,K.
TITLE BodyMap: human gene expression database
JOURNAL Unpublished (1995)
COMMENT Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.
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/note="One or more human adult tissue"

ORIGIN

Query Match 83.5%; Score 14.2; DB 6; Length 220;
Best Local Similarity 70.8%; Pred. No. 2.6e+03;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;